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"Structural and Mechanistic Analyses of TSC1/2 and Rheb 1/2-Mediated  
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## INTRODUCTION

The multi-protein kinase mTORC1 (mammalian target of rapamycin complex 1) regulates cell growth by coordinating upstream signals from growth factors, intracellular energy levels, and amino acid availability and is deregulated in diseases such as cancer and diabetes. The TSC1 and TSC2 proteins form a tumor suppressor complex, which acts as the main convergence point of many upstream regulatory signals in the mTORC1 signaling network, with the notable exception of amino acid availability. TSC1/2 is a GTPase activating protein (GAP) for the small GTPase Rheb, which binds directly to mTORC1 and stimulates its activity when GTP-bound. In response to growth factor withdrawal or energy stress, activation of TSC1/2 leads to mTORC1 inhibition by decreasing Rheb-GTP levels. In contrast to growth factor signaling, the mechanism of regulation of mTORC1 activity in response to amino acids is poorly understood and puzzling. Although Rheb is necessary for mTORC1 activation, high Rheb-GTP levels achieved by TSC2 loss or Rheb over-expression have different effects on amino acid signaling to mTORC1. While in TSC2 null state cells still respond to amino acid stimulation, Rheb over-expression makes the pathway insensitive to amino acid starvation. Although the mechanism of this difference is not known, it points to the presence of other unknown players in amino acid signaling. Given that the mTOR pathway is an important target in TSC treatment, understanding how impairment of TSC1/2 function results in the activation of mTORC1 is critical. In particular, there is a lack of information about the nutrient and growth factor input to the mTORC1 complex and the inhibitory mechanism of rapamycin. With the long-term goal of developing cancer therapeutics based on mTORC1 regulatory mechanisms, our structural and biochemical studies aim to find efficient means of regulating the mTOR signaling network. Therefore, we propose structural analyses of mTORC1 as well as mechanistic analyses of mTORC1 activation via Rheb.

## BODY

### Aim 1: Understand the role of Rheb-mediated phosphorylation of Raptor in the regulation of mTORC1

Previously, we showed that the Rag GTPases, which are also members of the Ras family of GTP-binding proteins, are amino acid-specific regulators of the mTORC1 pathway. Mammals express four Rag proteins-RagA, RagB, RagC, and RagD-that form heterodimers consisting of RagA or RagB with RagC or RagD. Rag heterodimers containing GTP-bound RagB interact with mTORC1, and amino acids induce the mTORC1-Rag interaction by promoting the loading of RagB with GTP, which enables it to directly interact with the raptor component of mTORC1. The activation of the mTORC1 pathway by amino acids correlates with the movement of mTORC1 from an undefined location to a compartment containing Rab7, a marker of both late endosomes and lysosomes. How the Rag proteins regulate mTORC1 is unknown, but, in cells expressing a RagB mutant that is constitutively bound to GTP (RagBGTP), the mTORC1 pathway is insensitive to amino acid starvation and mTORC1 resides in the Rab7-positive compartment even in the absence of amino acids. We previously proposed that amino acids promote the translocation of mTORC1-in a Rag-dependent fashion-to the surface of an endomembrane compartment, where mTORC1 can find its well-known activator, Rheb. However, in our recent study, we showed that amino acids induce the movement of mTORC1 to lysosomal membranes, where the Rag proteins reside. A complex encoded by the MAPKSP1, ROBLD3, and c11orf59 genes, which we term Ragulator, interacts with the Rag GTPases, recruits them to lysosomes, and is essential for mTORC1 activation. Constitutive targeting of mTORC1 to the lysosomal surface is sufficient to render the mTORC1 pathway amino acid insensitive and independent of Rag and Ragulator, but not Rheb, function. Thus, Rag-Ragulator-mediated translocation of mTORC1 to lysosomal membranes is the key event in amino acid signaling to mTORC1. Detailed descriptions of methodology and discussions can be found in Appendix 1.

### Aim 2: Elucidate the structural features of mTORC1 and its interacting proteins via X-ray crystallography, cryo-EM and SAXS

The study of mTORC1 phosphorylation of substrate sites has been greatly aided by pharmacological inhibitors of mTORC1, in particular rapamycin. Rapamycin, in complex with its

intracellular receptor FKBP12 (FK506-binding protein of 12 kDa), acutely inhibits mTORC1 by binding to the FRB domain of mTOR. Yet, the molecular mechanism of how this high-affinity interaction perturbs mTOR kinase activity and the fully assembled mTORC1 is currently unknown. Thus, a detailed knowledge of mTORC1 structure, including the organization of its components, has the potential to help understand the regulation of its kinase activity and to aid in the development of more effective mTORC1 inhibitors. Therefore, we determined the first three-dimensional (3D) structure of the fully assembled human mTORC1 in an active state by cryo-EM. To perform a cryo-EM analysis of mTORC1, microgram quantities of intact and active mTORC1 was necessary. The large size (1 MDa) and instability of mTORC1 made it difficult to obtain the purified complex for structural analysis. To address this issue, we devised a method to purify microgram quantities of intact and active human mTORC1. Keys to the successful purification of mTORC1 were the development of a human cell line stably expressing a tagged raptor subunit that incorporates into endogenous mTORC1, the identification of buffer conditions that minimize mTORC1 disintegration and/or aggregation during purification, and the implementation of tandem gel filtration chromatography steps to separate mTORC1 from other large contaminants. Purified mTORC1 consists of equimolar quantities of mTOR, raptor, and mLST8 and of PRAS40 at substoichiometric level. The kinase activity of purified mTORC1 toward S6K1 was sensitive to FKBP12-rapamycin and Torin1, an ATP-competitive inhibitor of mTOR. Negative-stain EM analysis of the purified complex revealed particles that were homogeneous in size and shape. Subsequently, we determined the three-dimensional (3D) structure of human mTORC1 by cryo-EM. This structure, together with labeling and biochemical studies, revealed the intricate organization of the components within mTORC1 and provides structural insights into the mechanism of its inhibition by FKBP12-rapamycin. In our recent publication, we reported that mTORC1 is an obligate dimer with an overall rhomboid shape and a central cavity. The dimeric interfaces are formed by interlocking interactions between the mTOR and raptor subunits. Extended incubation with FKBP12-rapamycin compromises the structural integrity of mTORC1 in a stepwise manner, leading us to propose a model in which rapamycin inhibits mTORC1-mediated phosphorylation of 4E-BP1 and S6K1 through different mechanisms. Based on these observations and our knowledge of the molecular organization of mTORC1, we proposed the following model for rapamycin-mediated inhibition of mTORC1. The initial binding of one FKBP12-rapamycin to mTORC1 causes a subtle conformational change in mTOR that weakens the mTOR-raptor interaction but does not suffice to disrupt the dimeric architecture. Moreover, the bound FKBP12-rapamycin likely occludes the binding of or blocks access to the active site for larger-sized substrates, such as S6K1. Over time, either amplified structural strain caused by the first FKBP12-rapamycin or, perhaps, the binding of a second rapamycin complex leads to a fast disintegration of the already “weakened” mTORC1 and the complete abolishment of 4E-BP1 phosphorylation. Therefore, our work suggests that in vitro rapamycin is an mTORC1 inhibitor that may work through at least two different modes. The fact that, within cells, rapamycin does not completely inhibit 4E-BP1 phosphorylation or mTORC1 stability suggests that cells contain buffering mechanisms that counter the effects of rapamycin on mTORC1 and that these are lost when mTORC1 is purified. Detailed descriptions of methodology and discussions can be found in Appendix 2.

#### KEY RESEARCH ACCOMPLISHMENTS

- Showed that mTORC1 translocates to the lysosomal surface in response to amino acid stimulation, and the Rag GTPases constitutively reside on the lysosomal surface
- Identified the Ragulator protein complex as novel Rag GTPase interacting proteins
- Showed that the Ragulator tethers the Rag GTPases to the lysosomal surface independent of amino acid availability, and is required for amino acid-induced mTORC1 lysosomal translocation
- Constitutively localized mTORC1 to the lysosomal surface and showed that the mTORC1 pathway activity becomes insensitive to amino acid starvation when on the lysosomal membrane
- Indicated lysosomes as the site of amino acid sensing in mammals for the first time
- Developed purification methods for human mTORC1 and raptor

- Characterized the structures of mTORC1 and free raptor by cryo-EM
- Analyzed the molecular architecture and subunit organization of mTORC1 based on antibody labeling and biochemical assays
- Provided structural insights into the mechanism of inhibition by rapamycin
- Developed a capillary isoelectric focusing technique under native conditions for the separation of mTOR complex isoforms and subcomplexes

## REPORTABLE OUTCOMES

- Publications:
  - Fonslow B.R., Kang S.A., Gestaut D.R., Graczyk B., Davis T.N., Sabatini D.M., Yates, J.R. Native Capillary Isoelectric Focusing for the Separation of Protein Complex Isoforms and Subcomplexes. *Anal. Chem.* **2010**, 82 (15), 6643-6651.
  - Yip, C.K., Murata, K., Walz, T., Sabatini, D.M., Kang, S.A. Structure of the human mTOR complex I and its implications for rapamycin inhibition. *Mol. Cell* **2010**, 38 (5), 768-774.
  - Sancak, Y., Bar-Peled, L., Zoncu, R., Markhard, A.L., Nada, S. and Sabatini, D.M. Ragulator-Rag Complex Targets mTORC1 to the Lysosomal Surface and Is Necessary for Its Activation by Amino Acids. *Cell* **2010**, 141 (2), 290-303.
- Patents applied:
  - SOLUBLE MTOR COMPLEXES AND MODULATORS THEREOF, International patent application number: PCT/US2009/005656, Based on U.S. patent application number: 61/185923, 61/196772 and 61/106411, Inventors: Nathanael Gray et al.
- Degrees awarded:
  - Yasemin Sancak, Ph.D. (May, 2010)

## CONCLUSION

Aim 1: Our recent findings, together with previous work showing that Rheb is required for amino acids to activate the mTORC1 pathway and can localize to late endosomes/lysosomes, is consistent with a model in which amino acids induce mTORC1 to associate with the endomembrane system of the cell and thus allow it to encounter its activator Rheb. In this model, the essential role of the Ragulator-Rag complex is to serve as an amino acid-regulated docking site for mTORC1 on lysosomal membranes. Ragulator, which consists of p14, p18, and MP1, is a Rag-interacting complex that is essential for amino acid signaling to mTORC1 and represents an additional critical component of the TORC1 signaling pathway in mammals and flies. p18 directly interacts with the Rag GTPases as well as with p14 and MP1 and so may serve as a scaffold to bring the Rag GTPases and MP1-p14 next to each other. In vitro we have not detected a direct interaction between the Rag GTPases and either MP1 or p14, but both proteins are, like p18, necessary for localizing the Rag GTPases to the lysosomal surface. p14 is required to maintain normal p18 expression levels, suggesting that within cells p14 and MP1 form a crucial part of the Ragulator structure. The proposed link between the Rag and Rheb GTPases in the regulation of the mTORC1 pathway provides an explanation for why activation of mTORC1 occurs only when activators of both Rheb (e.g., growth factors and energy) and the Rags (i.e., amino acids) are available.

Aim 2: For years, lack of meaningful structural information of the mTOR complexes has prevented us from answering a number of key questions concerning the mechanism of the action of the mTOR kinase, kinase-substrate interactions, and ultimately, its inhibition by FKBP12-rapamycin. In order to understand the overall architecture and subunit organization of this essential signaling complex, we have determined the three-dimensional structure of the fully assembled human mTORC1 by the high-resolution microscopy technique. Our analyses reveal that mTORC1 has a unique dimeric organization. The dimeric interfaces are formed by interlocking interactions between the multiple subunits. Extended incubation with the anti-cancer drug, rapamycin, compromises the structural integrity of mTORC1, thereby inhibiting the activity. Consequently, elucidating the structural features of mTORC1 and its inhibition by

rapamycin would provide insights into the mechanisms of complex formation/disruption, and potentially facilitate the rational design of mTOR inhibitors with improved efficacy and specificity.

#### APPENDICES

1. Sancak, Y., Bar-Peled, L., Zoncu, R., Markhard, A.L., Nada, S. and Sabatini, D.M. Ragulator-Rag Complex Targets mTORC1 to the Lysosomal Surface and Is Necessary for Its Activation by Amino Acids. *Cell* **2010**, 141 (2), 290-303.
2. Yip, C.K., Murata, K., Walz, T., Sabatini, D.M., Kang, S.A. Structure of the human mTOR complex I and its implications for rapamycin inhibition. *Mol. Cell* **2010**, 38 (5), 768-774.

# Ragulator-Rag Complex Targets mTORC1 to the Lysosomal Surface and Is Necessary for Its Activation by Amino Acids

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## SUMMARY

The mTORC1 kinase promotes growth in response to growth factors, energy levels, and amino acids, and its activity is often deregulated in disease. The Rag GTPases interact with mTORC1 and are proposed to activate it in response to amino acids by promoting mTORC1 translocation to a membrane-bound compartment that contains the mTORC1 activator, Rheb. We show that amino acids induce the movement of mTORC1 to lysosomal membranes, where the Rag proteins reside. A complex encoded by the *MAPKSP1*, *ROBLD3*, and *c11orf59* genes, which we term Ragulator, interacts with the Rag GTPases, recruits them to lysosomes, and is essential for mTORC1 activation. Constitutive targeting of mTORC1 to the lysosomal surface is sufficient to render the mTORC1 pathway amino acid insensitive and independent of Rag and Ragulator, but not Rheb, function. Thus, Rag-Ragulator-mediated translocation of mTORC1 to lysosomal membranes is the key event in amino acid signaling to mTORC1.

## INTRODUCTION

The multicomponent kinase mTORC1 (mammalian target of rapamycin complex 1) regulates cell growth by coordinating upstream signals from growth factors, intracellular energy levels, and amino acid availability and is deregulated in diseases such as cancer and diabetes (reviewed in [Guertin and Sabatini, 2007](#)). The TSC1 and TSC2 proteins form a tumor suppressor complex that transmits growth factor and energy signals to mTORC1 by regulating the GTP-loading state of Rheb, a Ras-related GTP-binding protein. When bound to GTP, Rheb interacts with and activates mTORC1 (reviewed in [Laplane and Sabatini, 2009](#))

and appears to be necessary for the activation of mTORC1 by all signals, including amino acid availability. In contrast, TSC1-TSC2 is dispensable for the regulation of mTORC1 by amino acids, and, in cells lacking TSC2, the mTORC1 pathway is sensitive to amino acid starvation but resistant to growth factor withdrawal ([Roccio et al., 2006](#); [Smith et al., 2005](#)).

Recently, the Rag GTPases, which are also members of the Ras family of GTP-binding proteins, were shown to be amino acid-specific regulators of the mTORC1 pathway ([Kim et al., 2008](#); [Sancak et al., 2008](#)). Mammals express four Rag proteins—RagA, RagB, RagC, and RagD—that form heterodimers consisting of RagA or RagB with RagC or RagD. RagA and RagB, like RagC and RagD, are highly similar to each other and are functionally redundant ([Hirose et al., 1998](#); [Sancak et al., 2008](#); [Schürmann et al., 1995](#); [Sekiguchi et al., 2001](#)). Rag heterodimers containing GTP-bound RagB interact with mTORC1, and amino acids induce the mTORC1-Rag interaction by promoting the loading of RagB with GTP, which enables it to directly interact with the raptor component of mTORC1 ([Sancak et al., 2008](#)). The activation of the mTORC1 pathway by amino acids correlates with the movement of mTORC1 from an undefined location to a compartment containing Rab7 ([Sancak et al., 2008](#)), a marker of both late endosomes and lysosomes ([Chavrier et al., 1990](#); [Luzio et al., 2007](#)). How the Rag proteins regulate mTORC1 is unknown, but, in cells expressing a RagB mutant that is constitutively bound to GTP (RagB<sup>GTP</sup>), the mTORC1 pathway is insensitive to amino acid starvation and mTORC1 resides in the Rab7-positive compartment even in the absence of amino acids ([Sancak et al., 2008](#)). We previously proposed that amino acids promote the translocation of mTORC1—in a Rag-dependent fashion—to the surface of an endomembrane compartment, where mTORC1 can find its well-known activator, Rheb. Here, we show that the lysosomal surface is the compartment where the Rag proteins reside and to which mTORC1 moves in response to amino acids. We identify the trimeric Ragulator protein complex as a new component of the mTORC1 pathway that interacts with the Rag GTPases, is



essential for localizing them and mTORC1 to the lysosomal surface, and is necessary for the activation of the mTORC1 pathway by amino acids. In addition, by expressing in cells a modified raptor protein that targets mTORC1 to the lysosomal surface, we provide evidence that supports our model of mTORC1 pathway activation by amino acids.

## RESULTS

### Amino Acids Cause the Translocation of mTORC1 to Lysosomal Membranes, Where the Rag GTPases Are Already Present

To better define the compartment to which mTORC1 moves upon amino acid stimulation, we costained human cells with antibodies to endogenous mTOR, raptor, or RagC, as well as to various endomembrane markers (data not shown). This revealed that in the presence, but not in the absence, of amino acids, mTOR and raptor colocalized with LAMP2 (Figures 1A and 1B), a well-characterized lysosomal marker (reviewed in Eskelinen, 2006). Amino acid stimulation also resulted in an appreciable increase in the average size of lysosomes, which, as determined by live-cell imaging, was most likely caused by lysosome-lysosome fusion (R.Z., unpublished data). The amino acid-induced movement of mTOR to the LAMP2-positive compartment depends on the Rag GTPases, as it was eliminated by the RNA interference (RNAi)-mediated cknockdown of RagA and RagB (Figures S1A and S1B available online). Endogenous RagC also colocalized extensively with LAMP2, but, unlike mTORC1, this colocalization was unaffected by amino acid availability (Figure 1C). Consistent with amino acids not regulating the interaction between RagC and RagA or RagB (Figure 1D), an antibody that recognizes RagA and RagB stained lysosomes in both amino acid-starved and replete cells (Figure 1E). Lastly, GFP-tagged wild-type and GTP-bound mutants of RagB (RagB<sup>GTP</sup>) and RagD (RagD<sup>GTP</sup>) behaved identically to their endogenous counterparts (Figures 1F and 1G). Thus, amino acids stimulate the translocation of mTORC1 to the lysosomal surface, where the Rag GTPases reside irrespective of their GTP-loaded states or amino acid availability. Given that mTORC1 interacts with the Rag heterodimers in an amino acid-dependent fashion (Sancak et al., 2008), the mTORC1 and Rag localization data are consistent with the Rag GTPases serving as an amino acid-regulated docking site for mTORC1 on lysosomes.

### The Translocation of mTORC1 to Lysosomes Does Not Depend on Growth Factors, Rheb, or mTORC1 Activity

The movement of mTORC1 to lysosomes is a specific response to amino acids. In wild-type mouse embryonic fibroblasts (MEFs), amino acids promoted the translocation of mTORC1 to lysosomes even when cells were cultured in the absence of serum (Figure S1C), a condition in which mTORC1 signaling, as detected by phosphorylated S6K1, is not active (Figure S1D). Conversely, in the absence of amino acids, neither serum stimulation nor constitutive activation of Rheb caused by the loss of TSC2 led to the lysosomal translocation of mTORC1 (Figure S1C). In both wild-type and TSC2 null MEFs, RNAi-mediated suppression of Rheb1 expression inhibited mTORC1 activation

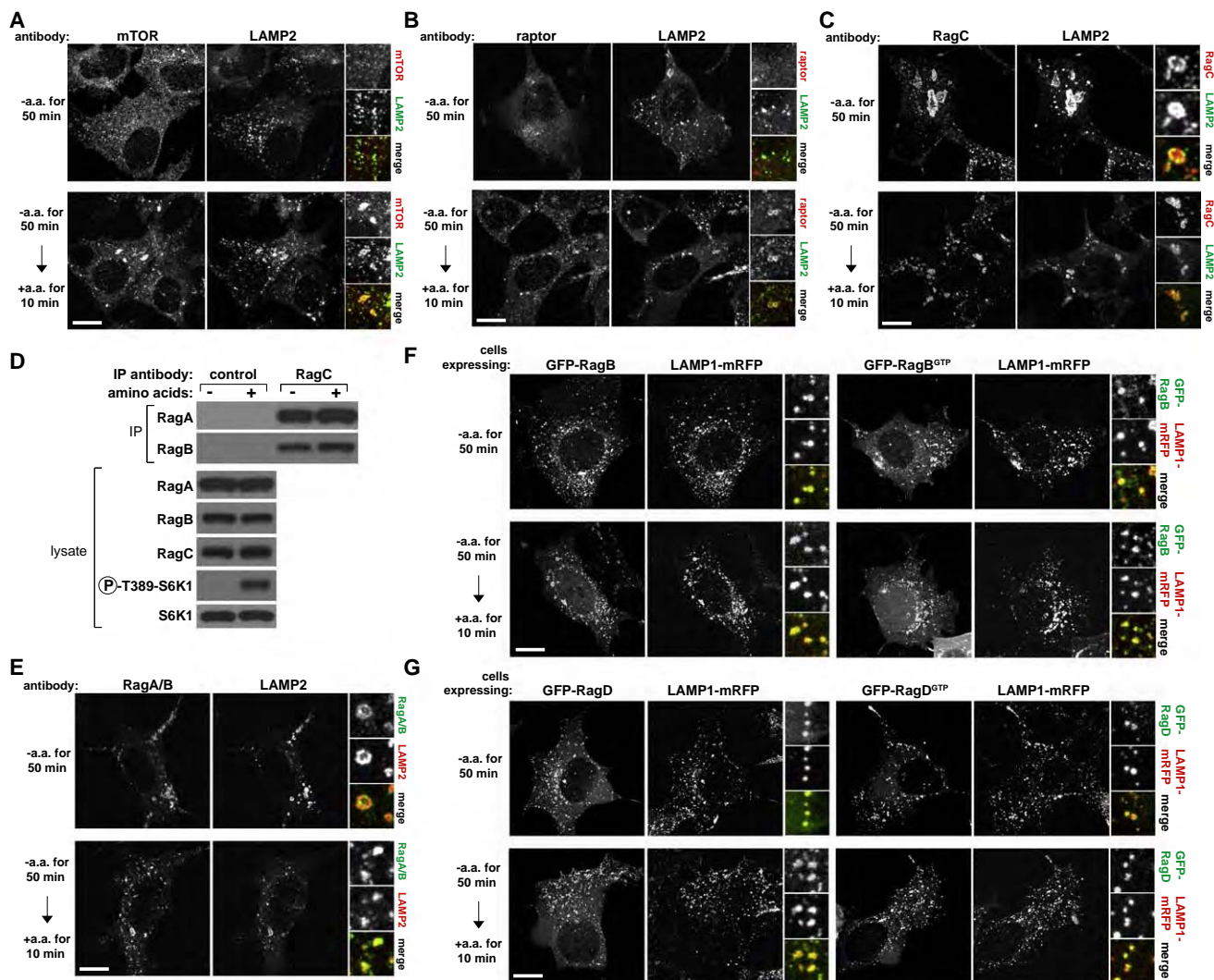
by amino acids (Figure S1E) but did not interfere with the amino acid-induced movement of mTOR to lysosomes (Figure S1F). Thus, the amino acid-induced translocation of mTORC1 to the lysosomal surface occurs independently of mTORC1 activity and does not require TSC2, Rheb, or growth factors.

### The Trimeric Regulator Complex Interacts with the Rag GTPases and Colocalizes with Them on Lysosomal Membranes

Inspection of the amino acid sequence of the Rag GTPases did not reveal any obvious lipid modification signals that might mediate Rag recruitment to lysosomal membranes. Thus, we pursued the possibility that unknown Rag-interacting proteins are needed to localize the Rag GTPases to lysosomes and play a role in mTORC1 signaling. To identify such proteins, we used protein purification approaches that have led to the discovery of other mTOR pathway components (see the Extended Experimental Procedures). Mass spectrometric analysis of anti-FLAG immunoprecipitates prepared from human HEK293T cells stably expressing FLAG-RagB or FLAG-RagD, but not FLAG-Rap2a, consistently revealed the presence of proteins encoded by the *MAPKSP1*, *ROBLD3*, and *c11orf59* genes (Figure 2A). Furthermore, the same proteins were also detected in immunoprecipitates of endogenous RagC but not control proteins like p53 or tubulin. Previous work indicates that these three small proteins interact with each other, localize to endosomes and lysosomes, and play positive roles in the MAPK pathway (Lunin et al., 2004; Nada et al., 2009; Schaeffer et al., 1998; Teis et al., 2002, 2006; Wunderlich et al., 2001). The proteins encoded by *MAPKSP1*, *ROBLD3*, and *c11orf59* have been called MP1, p14, and p18, respectively, and we use these names throughout this study. For convenience and because MP1, p14, and p18 are Rag and mTORC1 regulators (see below), we refer to the trimeric complex as the “Regulator.”

Orthologs of MP1, p14, and p18 are readily detectable in vertebrates as well as in *Drosophila* (Figure 2A), but extensive database searches did not reveal any potential orthologs in budding or fission yeast. The amino acid sequences of MP1, p14, and p18 reveal little about their function, and other than p14, which has a roadblock domain of unknown function (Koonin and Aravind, 2000), the proteins do not share sequence homology among themselves or with any other proteins in the databases besides their direct orthologs. In particular, they do not share any sequence similarity with the Ego1p or Ego3p, proteins, which interact with Gtr1p and Gtr2p (Dubouloz et al., 2005; Gao and Kaiser, 2006), the orthologs of the Rag proteins in budding yeast (Gao and Kaiser, 2006; Schürmann et al., 1995). The lysosomal localization of p18 requires its lipidation through N-terminal myristoylation and palmitoylation sites, and p18 likely serves as a platform for keeping MP1 and p14 on the lysosomal surface (Nada et al., 2009).

In humans, a mutation that leads to a partial reduction in the expression of p14 causes a pronounced growth defect so that individuals carrying the mutation are below the third percentile in age-adjusted height (Bohn et al., 2007). Furthermore, mice engineered to lack either p14 or p18 die around embryonic day 7–8 and exhibit severe growth retardation (Nada et al., 2009; Teis et al., 2006). Given the major role of the mTORC1



**Figure 1. mTORC1 Localizes to Lysosomal Membranes in an Amino Acid-Dependent Fashion while the Rag GTPases Are Constitutively Localized to the Same Compartment**

(A) Images of HEK293T cells coimmunostained for lysosomal protein LAMP2 (green) and mTOR (red). Cells were starved of and restimulated with amino acids for the indicated times before processing and imaging.

(B) Images of HEK293T cells coimmunostained for LAMP2 (green) and raptor (red). Cells were treated and processed as in (A).

(C) Images of HEK293T cells coimmunostained for LAMP2 (green) and RagC (red). Cells were treated and processed as in (A).

(D) RagC interacts with RagA and RagB independently of amino acid availability. RagC immunoprecipitates were prepared from HEK293T cells starved or stimulated with amino acids as in (A), and immunoprecipitates and lysates were analyzed by immunoblotting for the indicated proteins.

(E) Images of HEK293T cells coimmunostained for RagA/B (green) and LAMP2 (red). Cells were treated, processed, and imaged as in (A).

(F) GFP-RagB and GFP-RagB<sup>GTP</sup> colocalize with coexpressed LAMP1-mRFP independently of amino acid availability. HEK293T cells transfected with the indicated cDNAs were treated and processed as in (A).

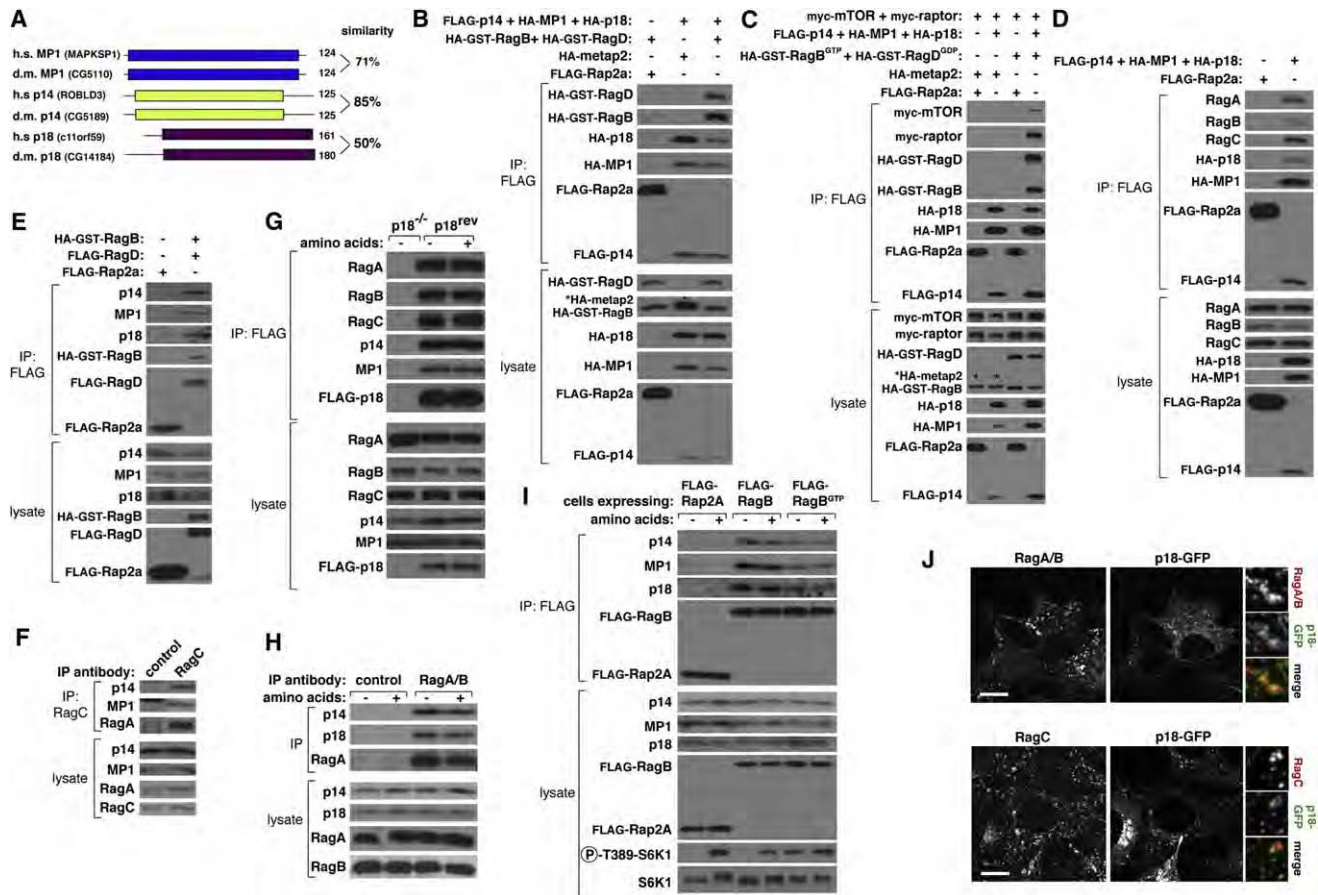
(G) GFP-RagD and GFP-RagD<sup>GTP</sup> colocalize with coexpressed LAMP1-mRFP independently of amino acid availability. HEK293T cells transfected with the indicated cDNAs were treated and processed as in (A).

In all images, insets show selected fields that were magnified five times and their overlays. Scale bars represent 10  $\mu$ m. See also Figure S1.

pathway in growth control, these loss-of-function phenotypes were of interest to us.

As an initial step in verifying our mass spectrometric identification of MP1, p14, and p18 as Rag-interacting proteins, we coexpressed them along with RagB and RagD in HEK293T cells and found that the Ragulator, but not the control Rap2A protein, coimmunoprecipitated both Rag GTPases but not the metap2

protein that has the same molecular weight as tagged RagB (Figure 2B). Furthermore, when coexpressed with a RagB mutant (RagB<sup>GTP</sup>) that binds constitutively to GTP, the Ragulator coimmunoprecipitated the mTORC1 components raptor and mTOR (Figure 2C), consistent with the GTP-loading of RagB promoting the interaction of the Rag heterodimers with mTORC1 (Sancak et al., 2008). Furthermore, endogenous RagA, RagB, and RagC



**Figure 2. The Trimeric Regulator Complex Interacts and Colocalizes with the Rag GTPases**

(A) Schematic amino acid sequence alignment of human MP1, p14, and p18 and their corresponding *Drosophila* orthologs.

(B) Recombinant epitope-tagged Regulator coimmunoprecipitates recombinant RagB and RagD. Anti-FLAG immunoprecipitates were prepared from HEK293T cells cotransfected with the indicated cDNAs in expression vectors and cell lysates and immunoprecipitates analyzed by immunoblotting for levels of indicated proteins. The \* indicates the band corresponding to the metap2 protein as it has the same apparent molecular weight as HA-GST-RagB.

(C) Recombinant Regulator coimmunoprecipitates mTORC1 when it is coexpressed with the GTP-bound mutant of RagB. HEK293T cells were cotransfected with the indicated cDNAs in expression vectors and analyzed as in (B). The \* indicates the bands corresponding to metap2 as it has the same apparent molecular weight as HA-GST-RagB.

(D) Recombinant Regulator co-immunoprecipitates endogenous RagA, RagB, and RagC. HEK293T cells were cotransfected with indicated cDNAs in expression vectors and anti-FLAG immunoprecipitates analyzed as in (B).

(E) Recombinant RagB-RagD heterodimers coimmunoprecipitate endogenous p14, MP1, and p18. HEK293T cells were cotransfected with indicated cDNAs in expression vectors and anti-FLAG immunoprecipitates analyzed as in (B).

(F) Endogenous RagC coimmunoprecipitates endogenous p14 and MP1. Anti-RagC immunoprecipitates were prepared from HEK293T cells and analyzed for the levels of the indicated proteins.

(G) Amino acids do not regulate the amounts of endogenous MP1, p14, RagA, or RagB that coimmunoprecipitate with recombinant p18. p18 null cells (p18<sup>-/-</sup>) or p18 null cells stably expressing FLAG-p18 (p18<sup>rev</sup>) were starved for amino acids for 50 min or starved and restimulated with amino acids for 10 min. After in-cell crosslinking, anti-FLAG immunoprecipitates were prepared from cell lysates and analyzed for the levels of the indicated proteins by immunoblotting.

(H) Amino acids do not affect the amounts of endogenous p14 and p18 that coimmunoprecipitate with endogenous RagA/B. HEK293T cells were treated as in (G), and anti-RagA/B immunoprecipitates were analyzed by immunoblotting for the indicated proteins.

(I) Endogenous Regulator coimmunoprecipitates with FLAG-RagB independently of amino acid availability and GTP-loading of RagB. HEK293T cells stably expressing FLAG-RagB or FLAG-RagB<sup>GTP</sup> were starved and restimulated with amino acids as in (G), and anti-FLAG immunoprecipitates were analyzed for the levels of indicated proteins.

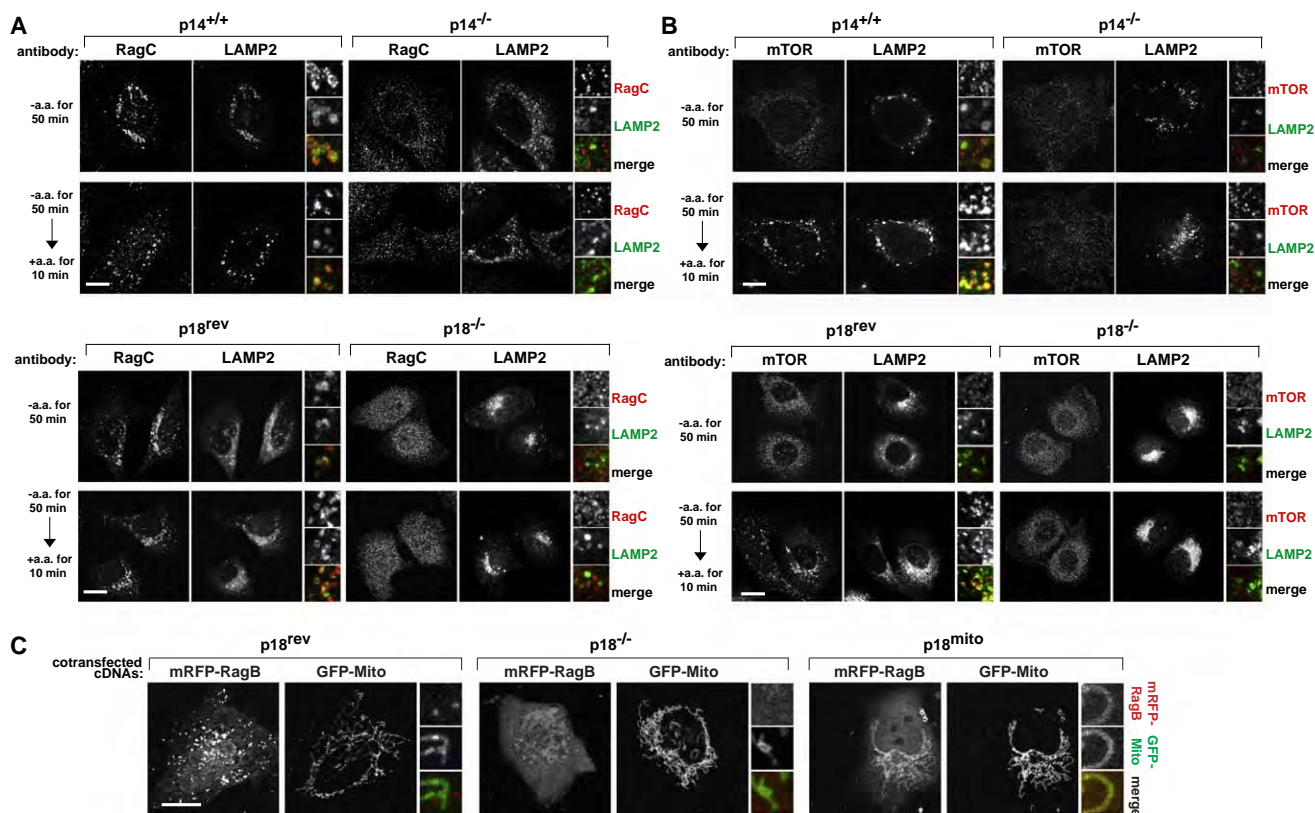
(J) The Rag GTPases colocalize with GFP-tagged p18. HEK293T cells were transfected with a cDNA encoding p18-GFP, processed for immunostaining for endogenous RagA/B or RagC, and imaged for the RagA/B (red) or RagC (red) signal as well as for p18-GFP fluorescence (green). Note that not all cells express p18-GFP. In all images, insets show selected fields that were magnified five times and their overlays. Scale bars represent 10  $\mu$ m.

See also Figure S2.

copurified with recombinant Regulator (Figure 2D), and endogenous Regulator components copurified with the recombinant RagB-RagD heterodimer (Figure 2E). Lastly, endogenous p14

and MP1 were present in immunoprecipitates prepared with an antibody directed against endogenous RagC that readily coimmunoprecipitates RagA (Figure 2F).





**Figure 3. The Ragulator Is Necessary to Localize the Rag GTPases and mTORC1 to Lysosomal Membranes**

(A) Images of p14 null or p18 null cells or their respective controls coimmunostained for RagC (red) and LAMP2 (green). Cells were starved of and restimulated with amino acids for the indicated times before processing for the immunofluorescence assay and imaging.

(B) Images of p14 null or p18 null cells or their respective controls coimmunostained for mTOR (red) and LAMP2 (green). Cells were treated and processed as in (A).

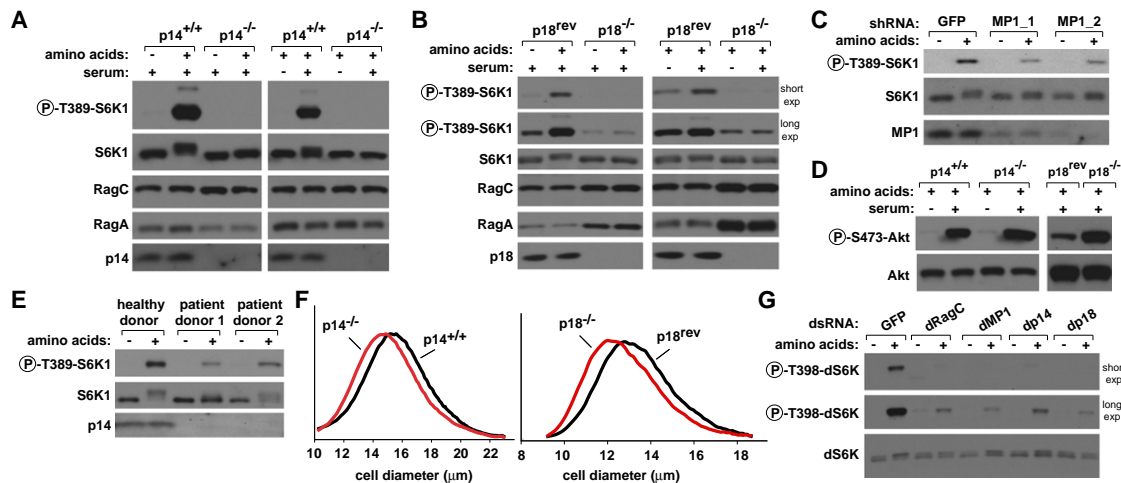
(C) Colocalization of mRFP-RagB (red) with GFP-Mito (green) in cells expressing mitochondrially localized p18. p18 null cells (p18<sup>-/-</sup>), or p18 null cells expressing wild-type p18 (p18<sup>rev</sup>) or mitochondrially localized p18 (p18<sup>mito</sup>), were transiently transfected with the indicated cDNAs in expression plasmids and imaged. In all images, insets show selected fields that were magnified five times and their overlays. Scale bars represent 10  $\mu$ m. See also Figure S3.

Amino acids did not appreciably regulate the interaction of recombinant p18 with endogenous p14, MP1, or the Rag GTPases (Figure 2G). Similarly, amino acids did not affect the interaction of endogenous Ragulator with endogenous Rag A/B (Figure 2H). The amounts of p14, p18, and MP1 that coimmunoprecipitated with the GTP-bound RagB mutant (RagB<sup>GTP</sup>) were slightly less than with wild-type RagB (Figure 2I). Because mTORC1 pathway activity is high in cells expressing RagB<sup>GTP</sup> (Sancak et al., 2008), the reduced Ragulator-Rag interaction in these cells may reflect a compensatory mechanism to reduce mTORC1 activity. To test whether the Rag GTPases interact with one or more Ragulator components directly, we performed in vitro binding assays between purified RagB-RagD heterodimers and individual Ragulator proteins. p18 interacted with RagB-RagD in vitro, but not with the Rap2a control protein (Figure S2A). In contrast, we did not detect a direct interaction between either p14 or MP1 and the Rag GTPases (data not shown), suggesting that p18 is the principal Rag-binding subunit of the Ragulator. Lastly, within HEK293T cells, GFP-tagged p18 colocalized with endogenous RagA/B and RagC (Figure 2J).

Collectively, these results show that the Ragulator interacts with the Rag GTPases and that a supercomplex consisting of Ragulator, a Rag heterodimer, and mTORC1 can exist within cells.

### Ragulator Localizes the Rag Proteins to the Lysosomal Surface and Is Necessary for the Amino Acid-Dependent Recruitment of mTORC1

Because the Rag GTPases interact with Ragulator and given the function of p18 in localizing MP1 and p14 to lysosomes (Nada et al., 2009), it seemed possible that the Ragulator is necessary for localizing the Rag proteins to the lysosomal surface. Indeed, in cells lacking p14 or p18 (Nada et al., 2009; Teis et al., 2006), endogenous RagC was localized in small puncta throughout the cytoplasm of the cells rather than to lysosomes (Figure 3A), the morphology of which was not obviously affected by the loss of either protein. In contrast, in p14<sup>+/+</sup> cells or p18 null cells reconstituted with wild-type p18 (p18<sup>rev</sup>), RagC constitutively colocalized with the LAMP2 lysosomal marker (Figure 3A). Analogous results were obtained in HEK293T cells with an RNAi-mediated reduction in MP1 expression (Figure S3A). Consistent



**Figure 4. Ragulator Null and -Depleted Cells are Highly Deficient in the Activation of mTORC1 Signaling by Amino Acids**

(A) p14 is necessary for the activation of the mTORC1 pathway by amino acids and serum. p14 null or control cells were starved of amino acids or serum for 50 min, or starved and restimulated with amino acids or serum for 10 min. Immunoblot analyses were used to measure the levels of the indicated proteins and phosphorylation states.

(B) p18 is necessary for the activation of the mTORC1 pathway by amino acids and serum. p18 null or control cells were treated and analyzed as in (A).

(C) Partial knockdown of MP1 blunts mTORC1 pathway activation by amino acids. HEK293T cells expressing a control shRNA or two distinct shRNAs targeting MP1 were starved for amino acids for 50 min, or starved and stimulated with amino acids for 10 min and analyzed as in (A).

(D) p14 and p18 are not necessary for mTORC2 pathway activity. p14 null or control cells were starved for serum, or starved and then restimulated with serum as in (A). p18 null or control cells were grown in complete media. Cell lysates were prepared and analyzed by immunoblotting for the levels of Akt1 and Akt phosphorylation at the S473 site phosphorylated by mTORC2.

(E) Decreased p14 expression impairs amino acid-induced mTORC1 activation in human cells. Cells derived from patients with lower p14 expression or healthy individuals were treated and analyzed as in (A).

(F) Cells lacking Ragulator are smaller than control cells. Cell size distributions of p14 null or p18 null cells are overlaid with those from corresponding control cells.

(G) Ragulator function is conserved in *Drosophila* cells. *Drosophila* S2 cells were transfected with a control dsRNA, or dsRNAs targeting dRagC, dMP1, dp14, or dp18, starved of amino acids for 90 min, or starved and restimulated with amino acids for 30 min. Levels of indicated proteins and phosphorylation states were analyzed by immunoblotting.

See also Figure S4.

with the essential role of the Rag proteins in the translocation of mTORC1 to the lysosomal surface (Figure S1), in cells lacking p14 or p18 or in HEK293T cells with p14, p18, or MP1 knockdowns, amino acids failed to induce lysosomal recruitment of mTOR, which was found throughout the cytoplasm in both amino acid-starved and -stimulated cells (Figure 3B, Figures S3B and S3D). Thus, all Ragulator subunits are required for lysosomal targeting of the Rag GTPases and mTORC1.

To determine whether Ragulator is sufficient to control the intracellular localization of the Rag proteins, it was necessary to target Ragulator to a location that is distinct from the lysosomal surface. As p18 binds both p14 and MP1 and is necessary for targeting them to the lysosomal surface (Nada et al., 2009), we chose to manipulate the intracellular localization of p18. To accomplish this, we generated a variant of p18, called p18<sup>mito</sup>, which lacks its N-terminal lipidation sites but is fused at its C terminus to the transmembrane region of OMP25, which is sufficient to target heterologous proteins to the mitochondrial surface (Nemoto and De Camilli, 1999). When expressed in p18 null cells, p18<sup>mito</sup> was associated with mitochondria, as verified by colocalization with the established mitochondrial protein Cytochrome c (Figure S3E). Remarkably, in the p18 null cells expressing p18<sup>mito</sup>, RFP-tagged RagB colocalized with the mitochondrial marker GFP-mito (Figure 3C). In contrast, RFP-RagB

did not colocalize with GFP-mito in p18 null cells (p18<sup>-/-</sup>) or p18<sup>rev</sup> cells and instead was present in a cytoplasmic or lysosomal pattern, respectively (Figure 3C). In cells expressing p18<sup>mito</sup>, mTORC1 activity remained very low and mTOR was not recruited to the mitochondria (Figures S3E and S3F), likely because the mitochondrial surface does not contain the machinery necessary to load the Rag GTPases with the appropriate nucleotides. These results indicate that the location of p18 is sufficient to define that of the Rag proteins and are consistent with Ragulator serving as a constitutive docking site on lysosomes for the Rag heterodimers, which, in amino acid-replete cells, have an analogous function for mTORC1.

#### Ragulator Is Necessary for TORC1 Activation by Amino Acids in Mammalian and *Drosophila* Cells

We employed the cells lacking p14 or p18 to determine whether Ragulator is necessary for mTORC1 activation by amino acids. Strikingly, in both p14 and p18 null cells, but not in control cells, amino acids were incapable of activating the mTORC1 pathway as detected by the phosphorylation of S6K1 (Figures 4A and 4B) and 4E-BP1 (Figure S4A). Similarly, cells derived from patients with a homozygous mutation in the p14 gene that causes a reduction in p14 expression (Bohn et al., 2007) showed a defect in amino acid-induced mTORC1 activation compared to cells

derived from a healthy donor (Figure 4E). In addition, autophagy, a process normally inhibited by mTORC1, was activated in p14 null cells, as detected by an increase compared to in control cells in the size and number of GFP-LC3-II puncta (Figures S4B and S4C). mTORC1 activity was also suppressed in HEK293T cells with RNAi-induced reductions in p14, p18, or MP1 levels (Figure 4C, Figure S3C). Consistent with the known requirement of amino acids and Rag function for growth factors to activate mTORC1 (Sancak et al., 2008), serum was also incapable of activating the mTORC1 pathway in cells null for p14 or p18 (Figures 4A and 4B). In contrast, no defect was observed in the level of S473 phosphorylation of Akt (Figure 4D). In fact, Akt phosphorylation was slightly higher in the p14 null and p18 null cells than in controls cells, which likely results from the lack of the well-appreciated inhibitory input from mTORC1 to the PI3K pathway in these cells (reviewed in Manning, 2004). As mTORC2 is the growth factor-regulated S473 kinase of Akt (Sarbasov et al., 2005), these results also indicate that the Ragulator does not play a detectable positive role in mTORC2 signaling. Interestingly, in the p18 null cells the expression of RagA and RagC was higher than in control cells (Figure 4B), suggesting that feedback signals in these cells may be trying to overcome the defect in mTORC1 activity by boosting Rag expression or that Ragulator also negatively controls Rag GTPase levels. Consistent with p18, p14, and MP1 forming a complex, the expression or stability of the Ragulator proteins seems to be coregulated because in cells that lack p14, p18 protein levels are also reduced, and, similarly, in cells that lack p18, p14 protein levels are also low (Figure S2B). A well-known function of the mTORC1 pathway is the positive regulation of cell growth, so that inhibition of the pathway leads to a reduction in cell size (reviewed in Laplante and Sabatini, 2009). Consistent with Ragulator being a positive component of the mTORC1 pathway, the p14 and p18 null cells were smaller in size than their respective controls (Figure 4F).

Many components of the TORC1 pathway, such as the Rag proteins, have conserved roles in mammalian and *Drosophila* cells (Kim et al., 2008; Sancak et al., 2008). RNAi-inducing double-stranded RNAs (dsRNAs) that target the *Drosophila* orthologs of MP1 (CG5110), p14 (CG5189), and p18 (CG14184) were as effective at blocking amino acid-stimulated activation of dTORC1 in *Drosophila* S2 cells as dsRNAs targeting dRagC (Figure 4G). Our loss-of-function experiments indicate that Ragulator is a component of the TORC1 pathway that, like the Rag GTPases, is essential for amino acids to activate TORC1 signaling in mammalian and *Drosophila* cells.

### Forced Targeting of mTORC1 to the Lysosomal Surface Eliminates the Amino Acid Sensitivity of the mTORC1 Pathway

The findings we have presented so far are consistent with the amino acid-induced movement of mTORC1 to the lysosomal surface being necessary for the activation of mTORC1 by amino acids. To test whether the placement of mTORC1 on lysosomal membranes is sufficient to mimic the amino acid input to mTORC1, it was necessary to force mTORC1 onto these membranes in the absence of amino acids. To accomplish this, we expressed in HEK293T cells modified raptor proteins that consist of epitope-tagged raptor fused to the intracellular target-

ing signals of Rheb1 or Rap1b, small GTPases that localize, in part, to the lysosomal surface (Pizon et al., 1994; Saito et al., 2005; Sancak et al., 2008). Because the targeting signals of these proteins are in their C-terminal tails, we added the last 15 or 17 amino acids of Rheb1 or Rap1b, respectively, to the C terminus of raptor (Figure 5A). For simplicity, we refer to these fusion proteins as raptor-Rheb15 and raptor-Rap1b17. As a control, we generated a raptor fusion protein that lacks the CAAX box of the Rheb1 targeting signal (raptor-Rheb15ΔCAAX) and so cannot associate with membranes (Buerger et al., 2006; Clark et al., 1997; Takahashi et al., 2005).

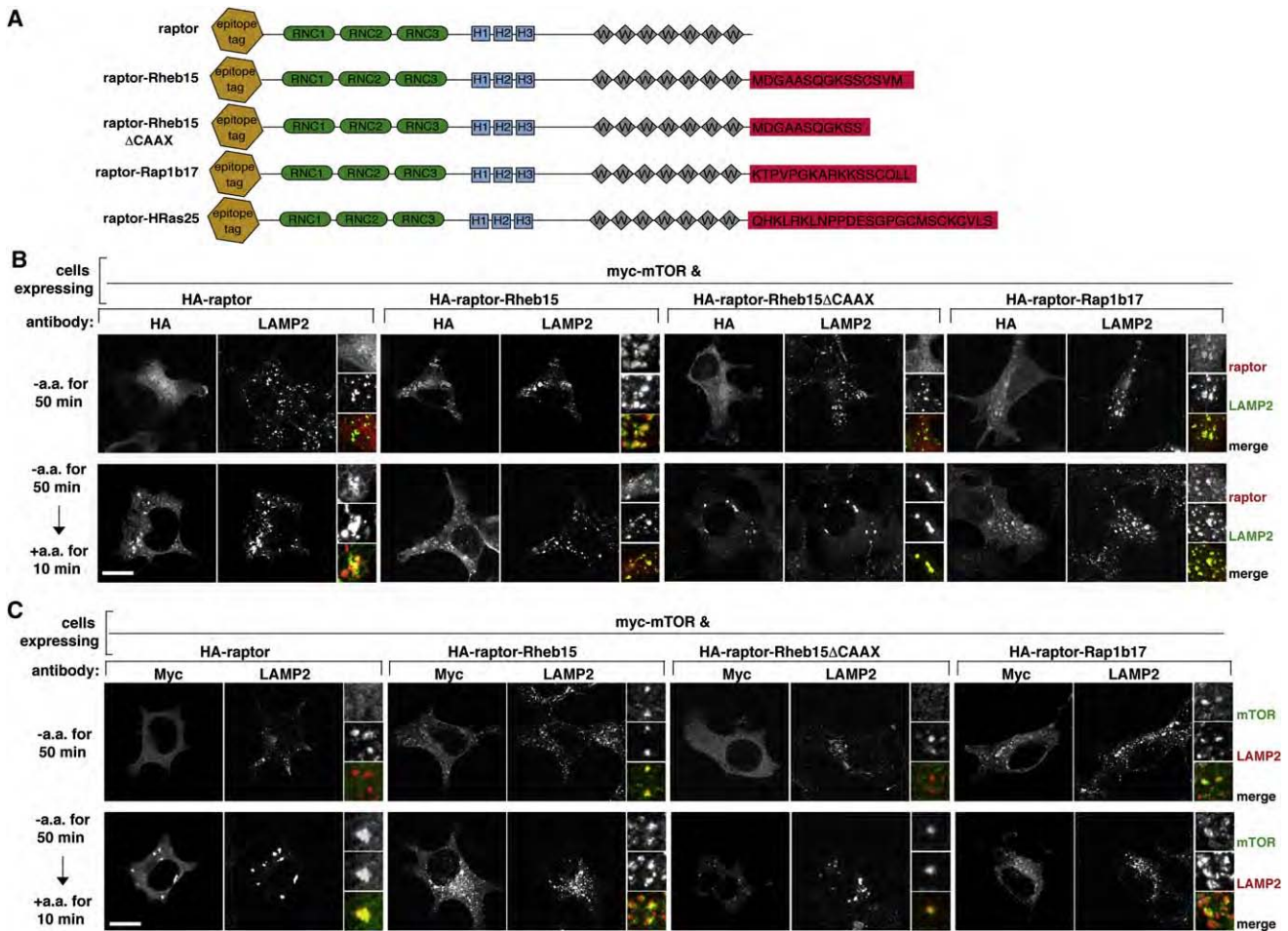
When expressed in cells together with myc-mTOR, raptor-Rheb15 and raptor-Rap1b17 localized to lysosomes in the presence or absence of amino acids, as judged by costaining with LAMP2 (Figure 5B). In contrast, raptor-Rheb15ΔCAAX behaved like wild-type raptor and localized to lysosomes only upon amino acid stimulation (Figure 5B). In all cases, the localization of the coexpressed myc-mTOR mirrored that of the wild-type or altered forms of raptor, indicating that C-terminal modifications of raptor do not perturb its interaction with mTOR (Figure 5C), which was confirmed in coimmunoprecipitation experiments (Figure S5A).

Remarkably, transient expression of raptor-Rheb15 or raptor-Rap1b17 in HEK293T cells was sufficient to render the mTORC1 pathway, as judged by the phosphorylation of S6K1, resistant to amino acid starvation (Figure 6A). In contrast, the expression of wild-type raptor or raptor-Rheb15ΔCAAX did not affect the amino acid sensitivity of the pathway (Figure 6A). In HEK293E cells, the expression of raptor-Rheb15 made S6K1 phosphorylation insensitive to amino acid starvation but did not affect its regulation by insulin (Figure 6B). Thus, lysosomal targeting of mTORC1 can substitute for the amino acid, but not growth factor, input to mTORC1. This is consistent with previous work showing that growth factors signal to mTORC1 in large part through the TSC1-TSC2-Rheb axis (reviewed in Laplante and Sabatini, 2009), and not through the Rag GTPases (Sancak et al., 2008).

To verify the effects of lysosomally targeted mTORC1 in a more physiological setting than that achieved by transient complementary DNA (cDNA) expression, we generated HEK293T cell lines stably expressing FLAG-tagged raptor-Rheb15 or wild-type raptor. In cells expressing the lysosomally targeted but not wild-type raptor, mTOR was always associated with lysosomes, irrespective of amino acids (Figure 6C). As with the transient expression of raptor-Rheb15, its stable expression rendered the mTORC1 pathway fully resistant to amino acid starvation (Figure 6D). Furthermore, under normal growth conditions, these cells had an increase in mTORC1 activity and were larger than controls (Figure 6E).

We next examined whether the targeting of mTORC1 to membranes other than lysosomal membranes could also eliminate the amino acid sensitivity of the mTORC1 pathway. This was not the case because although the stable expression of a raptor variant consisting of raptor fused to the last 25 amino acids of H-Ras (raptor-HRas25) (Figure 5A, Figure S5B) was sufficient to target a fraction of cellular mTOR to the plasma membrane (Figure 6C), it did not render the mTORC1 pathway resistant to amino acid starvation (Figure 6D).





**Figure 5. In Cells Expressing Raptor Variants Fused to the Targeting Signals of Rheb1 or Rap1b, mTORC1 Localizes to Lysosomal Membranes in an Amino Acid-Independent Fashion**

(A) Schematic of raptor fusion proteins that target mTORC1 to lysosomal membranes (raptor-Rheb15; raptor-Rap1b17) or to the plasma membrane (Raptor-HRas25) as well as proteins used as controls (wild-type raptor; raptor-Rheb15ΔCAAX).

(B) Images of amino acid starved or replete cells expressing lysosomally targeted or control HA-tagged raptor proteins and coimmunostained for the HA epitope (red) and endogenous LAMP2 (green). HEK293T cells were transfected with the indicated cDNAs, starved of and restimulated with amino acids for the indicated times, and processed in the immunofluorescence assay.

(C) Images of amino acid starved or replete cells coexpressing myc-mTOR and the indicated raptor fusion proteins and coimmunostained for the myc epitope (green) and endogenous LAMP2 (red). HEK293T cells were co-transfected with the indicated cDNAs and treated and processed as in (B).

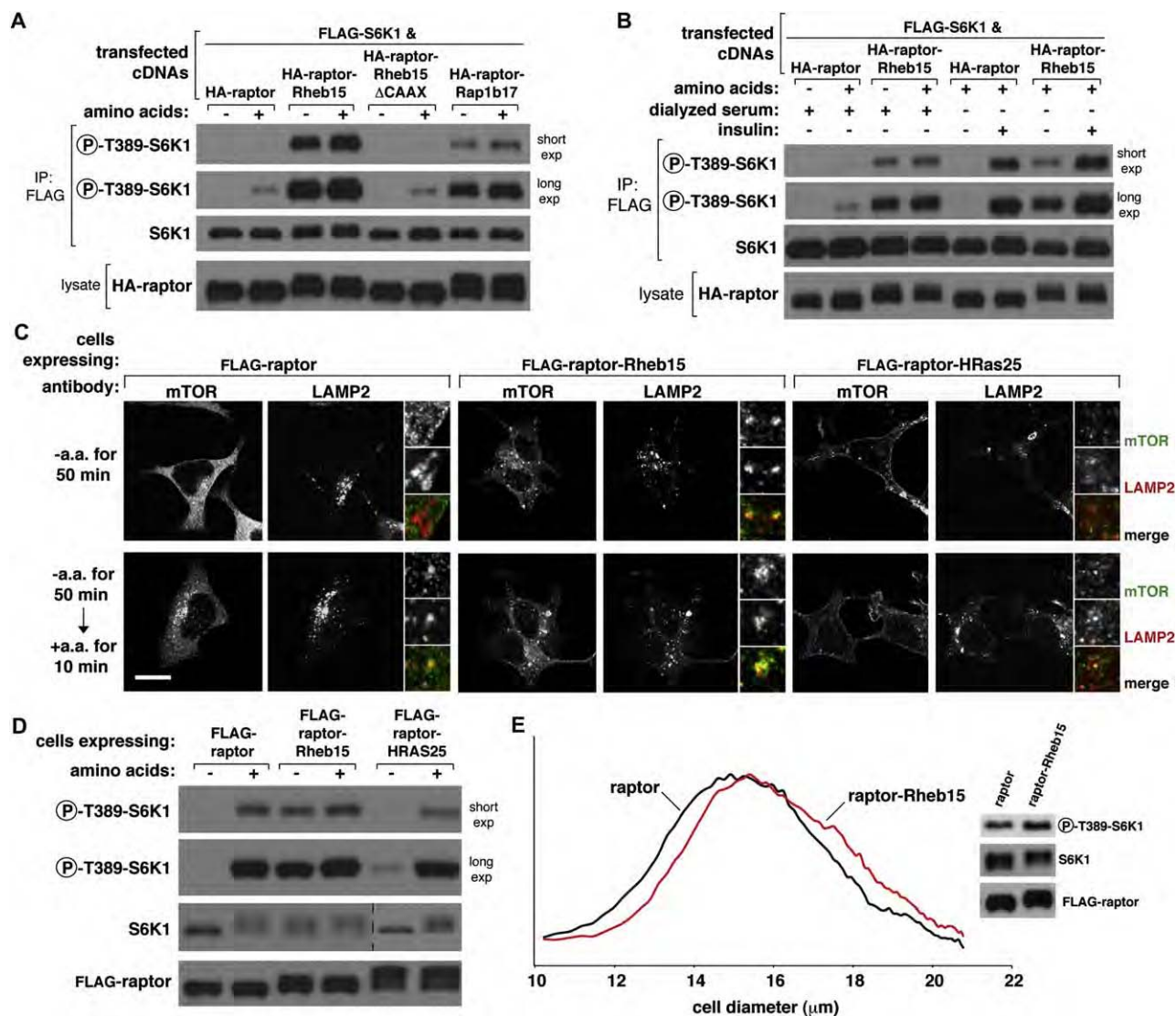
In all images, insets show selected fields that were magnified five times and their overlays. Scale bars represent 10  $\mu$ m.

### Forced Targeting of mTORC1 to the Lysosomal Surface Eliminates the Requirement in mTORC1 Signaling for Rag and Ragulator, but Not Rheb, Function

The ability to constitutively localize mTORC1 to lysosomal membranes enabled us to probe in more detail the role of the Rag and Rheb GTPases, as well as Ragulator, in the activation of mTORC1 by amino acids. We hypothesized that if the major role of the Rag GTPases is to allow mTORC1 to localize to lysosomes, then in cells that express raptor-Rheb15, mTORC1 activity should be independent of Rag function. Indeed, while in control cells the RNAi-mediated knockdown of both RagA and RagB strongly blunted the activation of mTORC1 by amino acids, it did not reduce the amino acid-insensitive mTORC1 activity observed in raptor-Rheb15-expressing cells

(Figure 7A). As an additional approach to inhibit Rag function, we exploited the fact that coexpression of a GDP-bound RagB mutant (RagB<sup>GDP</sup>) and a GTP-bound RagD mutant (RagD<sup>GTP</sup>) eliminates mTORC1 pathway activity within cells (Kim et al., 2008; Sancak et al., 2008). Expression of RagB<sup>GDP</sup>-RagD<sup>GTP</sup> completely prevented mTORC1 activation by amino acids in control cells but had no effect on the amino acid-insensitive mTORC1 activity of cells expressing raptor-Rheb15 (Figure 7B).

If the main function of Ragulator in the mTORC1 pathway is to localize the Rag GTPases to the lysosomes, then it should be possible to reactivate the mTORC1 pathway in Ragulator null cells by expressing raptor-Rheb15. Remarkably, the stable expression of raptor-Rheb15, but not wild-type raptor, in p14 or p18 null cells reactivated mTORC1 signaling and made it



**Figure 6. Constitutive Association of Raptor with Lysosomal Membranes, but Not the Plasma Membrane, Is Sufficient to Make the mTORC1 Pathway Insensitive to Amino Acid Starvation**

(A) The mTORC1 pathway is not sensitive to amino acid starvation in cells that express lysosomally targeted but not control raptor proteins. HEK293T cells were cotransfected with the indicated cDNA expression plasmids and starved of amino acids for 50 min or starved and restimulated with amino acids for 10 min. Cell lysates and anti-FLAG-S6K1 immunoprecipitates were analyzed by immunoblotting for the levels of the indicated proteins and phosphorylation states.

(B) The mTORC1 pathway is sensitive to serum starvation and insulin stimulation in cells that express lysosomally targeted as well as control raptor proteins. HEK293E cells were cotransfected with the indicated cDNA expression plasmids, starved of amino acids for 50 min, or starved and restimulated with amino acids for 10 min. Duplicate cultures were starved of serum for 50 min or starved and stimulated with insulin for 10 min. Cell lysates and anti-FLAG-S6K1 immunoprecipitates were analyzed by immunoblotting for the levels of the indicated proteins and phosphorylation states.

(C) Images of cells stably expressing FLAG-raptor, FLAG-raptor-Rheb15, or FLAG-raptor-HRAS25 and coimmunostained for endogenous mTOR (green) and endogenous LAMP2 (red). HEK293T cells stably expressing the indicated proteins were treated as in (A) for the indicated times before processing in the immunofluorescence assay. In all images, insets show selected fields that were magnified five times and their overlays. The scale bar represents 10  $\mu$ m.

(D) Targeting of mTORC1 to the lysosomal but not the plasma membrane makes the mTORC1 pathway insensitive to amino acid starvation. HEK293T cells stably expressing FLAG-raptor, FLAG-raptor-Rheb15, or FLAG-raptor-HRAS25 were treated as in (A) and analyzed by immunoblotting for the levels of the indicated proteins and phosphorylation states.

(E) Targeting of mTORC1 to the lysosomal membrane increases cell size and pathway activity in cells under normal growth conditions. Cell size distributions of cells that stably express FLAG-raptor or FLAG-raptor-rheb15 as well as immunoblot analyses of the mTORC1 pathway in the same cells are shown.



insensitive to amino acid deprivation (Figures 7C and 7D). Furthermore, expression of raptor-Rheb15 in the p18 null cells was sufficient to increase their size (Figure 7E). In contrast to the results observed with the Rag GTPases and Ragulator, RNAi-mediated suppression of Rheb1 blocked amino acid-induced mTORC1 activation in cells expressing raptor-Rheb15 to the same extent as it did in control cells (Figure 7F).

To test whether the presence of mTORC1 and Rheb on the same membrane compartment is sufficient to render the mTORC1 pathway insensitive to amino acid levels, we generated cells in which mTORC1 and Rheb are both present on the plasma membrane. To accomplish this, we prepared a Rheb1 variant, called Rheb1-HRas25, that localizes to the plasma-membrane (Figure S5C) because it contains the C-terminal 25 amino acids of H-Ras instead of the normal Rheb1 localization signal. When Rheb1-HRas25 was stably coexpressed with raptor-HRas25, but not wild-type raptor, the mTORC1 pathway became insensitive to amino acid starvation (Figure 7G). Importantly, mTORC1 signaling remained amino acid-sensitive in cells in which either Rheb or mTORC1, but not both, was targeted to the plasma membrane (Figure 7G).

## DISCUSSION

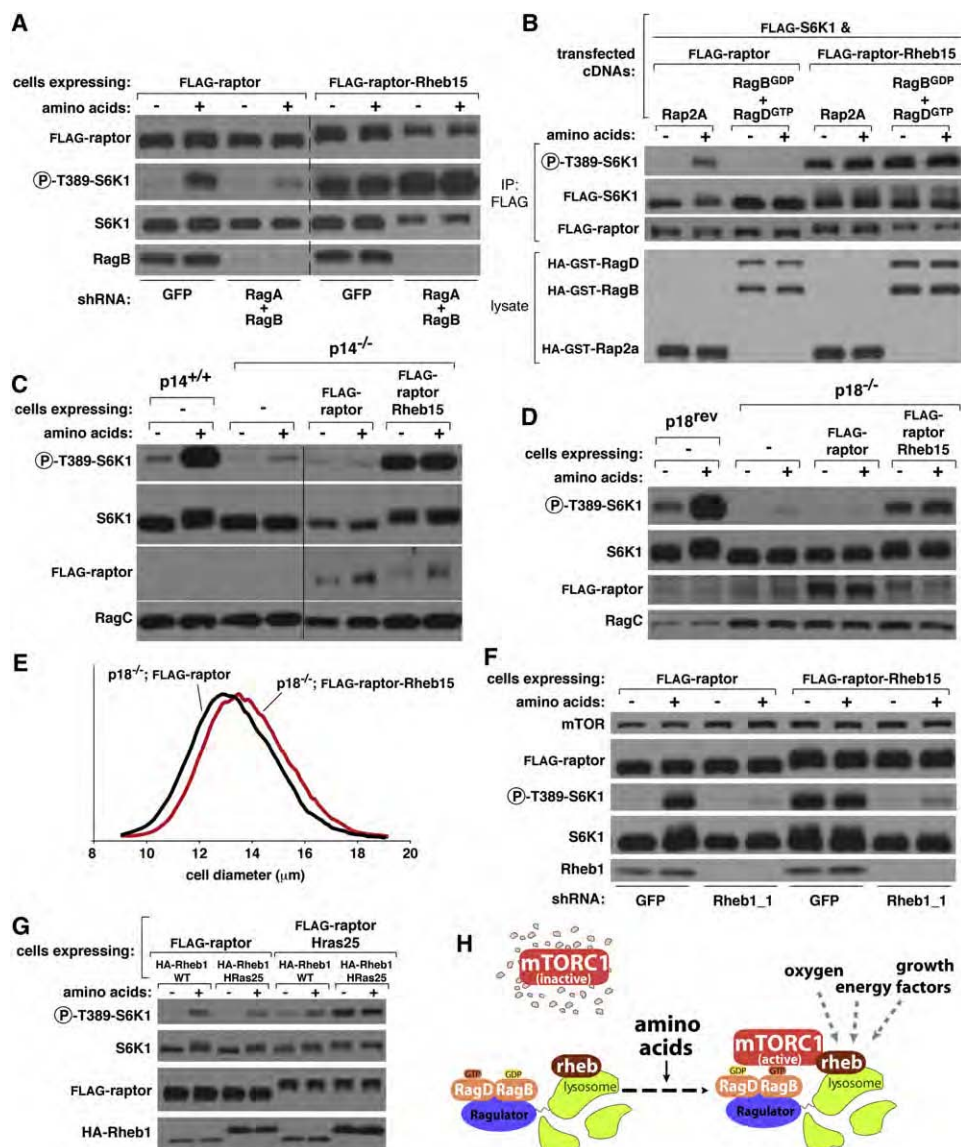
Our findings, together with previous work showing that Rheb is required for amino acids to activate the mTORC1 pathway (Roccio et al., 2006; Smith et al., 2005) and can localize to late endosomes/lysosomes (Saito et al., 2005; Sancak et al., 2008), is consistent with a model in which amino acids induce mTORC1 to associate with the endomembrane system of the cell and thus allow it to encounter its activator Rheb. In this model, the essential role of the Ragulator-Rag complex is to serve as an amino acid-regulated docking site for mTORC1 on lysosomal membranes (see schematic in Figure 7H). The proposed link between the Rag and Rheb GTPases in the regulation of the mTORC1 pathway provides an explanation for why activation of mTORC1 occurs only when activators of both Rheb (e.g., growth factors and energy) and the Rags (i.e., amino acids) are available. For technical reasons (Buerger et al., 2006; Sancak et al., 2008), it has not been possible to determine the intracellular localization of endogenous Rheb, and work using overexpressed GFP-tagged Rheb1 has placed it on various endomembrane compartments, including endosomes and lysosomes (Buerger et al., 2006; Saito et al., 2005; Sancak et al., 2008; Takahashi et al., 2005). Our results suggest that at some point in its life cycle, Rheb must traverse the lysosomal surface in order to encounter mTORC1, and so in our model we have chosen to place Rheb on this compartment (Figure 7H). However, at any given time only a small fraction of cellular Rheb may actually be on the lysosomal surface, or, alternatively, some of the mTORC1 within the cell may move to a nonlysosomal endomembrane compartment that also contains Rheb. These issues will only be answered once a definitive location for endogenous Rheb can be determined.

The trimeric p14, p18, and MP1 protein complex, which we call Ragulator, is a Rag-interacting complex that is essential for amino acid signaling to mTORC1 and represents an additional critical component of the TORC1 signaling pathway in

mammals and flies. p18 directly interacts with the Rag GTPases (Figure S2A) as well as with p14 and MP1 (Nada et al., 2009) and so may serve as a scaffold to bring the Rag GTPases and MP1-p14 next to each other. In vitro we have not detected a direct interaction between the Rag GTPases and either MP1 or p14, but both proteins are, like p18, necessary for localizing the Rag GTPases to the lysosomal surface. p14 is required to maintain normal p18 expression levels (Figure S2B), suggesting that within cells p14 and MP1 form a crucial part of the Ragulator structure. Given the nonspecific nature of the p14 and p18 names, in the future it may be best to rename these proteins, perhaps to names that reflect their essential roles in the mTORC1 pathway.

The location of the Rag GTPases, the Ragulator, and mTORC1 on the lysosomal surface implicates this organelle as the site of a yet to be discovered sensing system that signals amino acid availability to the Ragulator-Rag complex. The lysosomal location of the amino acid sensing branch of the mTORC1 pathway is consistent with increasing evidence that lysosomes, and their yeast counterparts, vacuoles, are at the nexus of amino acid metabolism within cells. Lysosomes are a major site of protein degradation and amino acid recycling, and vacuoles store amino acids at high concentrations (reviewed in Li and Kane, 2009). Thus, mTORC1 and its regulators may reside on the lysosomal surface so as to sense a currently unknown aspect of lysosomal function that reflects the intracellular pools of amino acids.

It is interesting to consider the differences and similarities between the still poorly understood amino acid signaling mechanisms employed by the mTORC1 and yeast TORC1 pathways. Consistent with previous work in mammalian cells (Sancak et al., 2008), the Gtr1p-Gtr2p heterodimer that is orthologous to RagA/B-RagC/D interacts with yeast TORC1 when Gtr1p is GTP loaded (Binda et al., 2009). TORC1 and the Gtr proteins are located on the surface of the vacuole (Berchtold and Walther, 2009; Binda et al., 2009), the yeast equivalent of lysosomes, but, unlike in mammals, yeast TORC1 does not leave the vacuolar surface upon amino acid deprivation although amino acids do control the interaction of TORC1 with Gtr1p-Gtr2p (Binda et al., 2009). This finding suggests that there must be a distinct mechanism for retaining TORC1 at the vacuolar surface and that in yeast the interaction between TORC1 and Gtr1p-Gtr2p serves other purposes besides controlling the intracellular location of TORC1. In contrast, our current work argues that in mammals, the main role of the Rag GTPase and the associated Ragulator complex is to control the association of mTORC1 with the cellular endomembrane system, in particular, lysosomes. Rheb, which is essential for the activation of mTORC1 by all upstream signals, does not appear to be part of the TORC1 pathway in yeast (reviewed in Berchtold and Walther, 2009). As we suggest that the Rag-dependent and amino acid-regulated translocation of mTORC1 to the lysosomal surface may ultimately be a mechanism for controlling the access of mTORC1 to Rheb, the absence of Rheb in the yeast TORC1 pathway may make regulation of TORC1 localization unnecessary. That known Rag- and Gtr-interacting proteins share no sequence homology also suggests that the mechanisms through which the Rag and Gtr GTPases regulate mTORC1 and yeast TORC1, respectively, have diverged. Although it is clear that



**Figure 7. Targeting of mTORC1 to the Lysosomal Surface Makes the Activity of the mTORC1 Pathway Independent of Rag and Ragulator, but Not Rheb, Function**

(A) In cells that express FLAG-raptor-Rheb15, mTORC1 pathway activity is independent of Rag GTPase function. Lysates of HEK293T cells expressing FLAG-raptor or FLAG-raptor-Rheb15 were analyzed by immunoblotting for the indicated proteins and phosphorylation states after disruption of Rag function by RNAi-mediated knockdown of RagA and RagB. Cells were starved of amino acids for 50 min or starved and restimulated with amino acids for 10 min before lysis.

(B) In cells that express FLAG-raptor-Rheb15, mTORC1 pathway activity is independent of Rag GTPase function. Lysates of HEK293T cells expressing FLAG-raptor or FLAG-raptor-Rheb15 were analyzed as in (A) after disruption of Rag function by expression of the dominant negative RagB<sup>GDP</sup>-RagD<sup>GTP</sup> heterodimer. Cells were treated and processed as in (A).

(C) Stable expression of FLAG-raptor-Rheb15 but not FLAG-raptor in p14 null cells is sufficient to reactivate the mTORC1 pathway and make it insensitive to amino acid starvation. Cells stably expressing the indicated proteins were treated and analyzed as in (A).

(D) Stable expression of FLAG-raptor-Rheb15 but not FLAG-raptor in p18 null cells is sufficient to reactivate the mTORC1 pathway and make it insensitive to amino acid starvation. Cells stably expressing the indicated proteins were treated and analyzed as in (A).

(E) In p18 null cells expression of raptor-Rheb15, but not wild-type raptor, increases cell size. Cell size distributions of p18 null cells that stably express FLAG-raptor or FLAG-raptor-Rheb15 are shown.

(F) In cells that express FLAG-raptor-Rheb15, the activity of the mTORC1 pathway is still Rheb dependent. Lysates of HEK293T cells that stably express FLAG-raptor or FLAG-raptor-Rheb15 were analyzed by immunoblotting for the indicated proteins and phosphorylation states after disruption of Rheb function by an RNAi-mediated knockdown of Rheb1. Cells were treated as in (A).

(G) Coexpression of plasma membrane-targeted raptor and plasma membrane-targeted Rheb1 renders the mTORC1 pathway insensitive to amino acid starvation. HEK293T cells stably expressing the indicated proteins were treated and analyzed as in (A).

the Ragulator and EGO complexes both control the intracellular localization of the Rag (this paper) and Gtr (Gao and Kaiser, 2006) GTPases, respectively, whether these complexes have additional functions remains to be determined.

Previous studies suggest that MP1-p14-p18 complex plays an adaptor role in the MAP kinase (MAPK) pathway (reviewed in Dard and Peter, 2006), and our current findings do not contradict these results. However, considering the very strong inhibition of the mTORC1 pathway that occurs in cells lacking p14 or p18, it seems possible that some of the impairment in MAPK signaling observed in those cells reflects an altered feedback signaling from Akt to the MAPK pathway. For example, in Ragulator null cells, Akt is slightly activated, almost certainly because the well-known inhibitory signal from mTORC1 to PI3K is absent. As Akt suppresses MAPK signaling by phosphorylating and inhibiting Raf (Zimmermann and Moelling, 1999), it is conceivable that the activation of Akt that occurs in Ragulator null cells could account, at least in part, for the inhibition of MAPK signaling that has been observed in these cells.

Mice lacking either p14 or p18 die around embryonic day 7.5–8 and have obvious growth defects (Nada et al., 2009; Teis et al., 2006). We would not be surprised if, when generated, mice lacking the Rag proteins die at around the same age and present similar defects. On the other hand, mice lacking the core mTORC1 component raptor die earlier (before embryonic day 6.5) than p14 and p18 null mice (Guertin et al., 2006). This may be expected because although loss of p14 or p18 completely blocks mTORC1 activation by amino acids, cells lacking the Ragulator proteins are likely to retain a low residual level of mTORC1 activity that may be sufficient to support development further than in embryos completely lacking mTORC1 function. Lastly, our results suggest that the strong growth retardation observed in humans with a mutation that reduces p14 expression (Bohn et al., 2007) is a result of partial suppression of the mTORC1 pathway. If this turns out to be the case, it would represent the first human example of a loss-of-function mutation in a positive component of the mTORC1 pathway.

## EXPERIMENTAL PROCEDURES

### Cell Lines and Tissue Culture

HEK293E cells, HEK293T cells, and TSC2<sup>+/+</sup>, TSC2<sup>-/-</sup>, p14<sup>+/+</sup>, and p14<sup>-/-</sup> MEFs were cultured in Dulbecco's modified Eagle's medium (DMEM) with 10% inactivated fetal calf serum. p18<sup>rev</sup>, p18<sup>mito</sup>, and p18<sup>-/-</sup> cells were cultured in DMEM with 10% fetal bovine serum. HEK293E and HEK293T cells express E1a and SV40 large T antigen, respectively. In HEK293E, but not HEK293T, cells the mTORC1 pathway is strongly regulated by serum and insulin (Sancak et al., 2007). TSC2<sup>-/-</sup>, p53<sup>-/-</sup>, and TSC2<sup>+/+</sup>, p53<sup>-/-</sup> MEFs were kindly provided by David Kwiatkowski (Harvard Medical School). The HEK293E cell line was kindly provided by John Blenis (Harvard Medical School). p14<sup>-/-</sup> and control MEFs were kindly provided by Lukas A. Huber (Innsbruck Medical University) and described are in Teis et al. (2006). p18<sup>-/-</sup> cells are epithelial in nature, and p18<sup>rev</sup> cells are p18<sup>-/-</sup> cells in which wild-type p18 has been re-expressed (Nada et al., 2009). Patient-derived cells with a homozygous mutation in the *ROBLD3* (p14) gene 3' untranslated region

and control healthy donor-derived cells were kindly provided by Christoph Klein (Universität München) and have been described in Bohn et al. (2007)

### Amino Acid and Serum Starvation and Stimulation of Cells

Serum and/or amino acid starvation of HEK293T cells, HEK293E cells, p14 null and control cells, p18 null and control cells, MEFs, and patient-derived and healthy donor-derived cells were performed essentially as described (Sancak et al., 2008). Serum was dialyzed against phosphate-buffered saline (PBS) in dialysis cassettes (Thermo Scientific) having a 3500 molecular weight cutoff.

### Preparation of Cell Lysates and Immunoprecipitations

Cell lysate preparation, cell lysis, and immunoprecipitations were done as described in the Extended Experimental Procedures.

For cotransfection experiments, 2,000,000 HEK293T or HEK293E cells were plated in 10 cm culture dishes. Twenty-four hours later, cells were transfected with the indicated plasmids as follows: 50 ng or 1500 ng myc-mTOR in pRK5; 20 ng or 500 ng HA-, myc-, or FLAG-Raptor in pRK5 or pLJM1 with or without the targeting signals; 100 ng HA-GST-Rap2a in pRK5; 100 ng HA-GST-Rheb1 in pRK5; 100 ng HA-GST-RagB in pRK5; 100 ng HA-GST-RagD in pRK5; 1 ng FLAG-S6K1 in pRK7; 50 ng or 600 ng HA- or FLAG-p14 in pRK5; 75 ng or 600 ng HA-MP1 in pRK5; and 50 ng or 800 ng HA-p18 in pRK5. The total amount of plasmid DNA in each transfection was normalized to 2 µg with empty pRK5.

### Cell Size Determinations

For measurement of cell size, 2,000,000 HEK293T cells or 200,000 of other cell types were plated into 10 cm culture dishes. Twenty-four hours later, the cells were harvested by trypsinization in a 4 ml volume and diluted 1:20 with counting solution (Isoton II Diluent, Beckman Coulter). Cell diameters were determined with a particle size counter (Coulter Z2, Beckman Coulter) running Coulter Z2 AccuComp software.

### Mammalian Lentiviral shRNAs and cDNAs

Lentiviral short hairpin RNAs (shRNAs) targeting human Rheb1, RagB, and RagC have been described (Sancak et al., 2008). Lentiviral shRNAs targeting mouse Rheb1 and human p14 were obtained from Sigma-Aldrich. Lentiviral shRNAs targeting the messenger RNA for human MP1 and human p18 were cloned into pLKO.1 vector as described (Sarbasov et al., 2005). The target sequences are provided in the Extended Experimental Procedures. Virus generation and infection was done as previously described (Sancak et al., 2008).

Raptor was cloned into the AgeI and BamHI sites of a modified pLKO.1 vector (pLJM1) (Sancak et al., 2008) with or without the Rheb1, Rap1b, and HRas targeting signals or cloned into the pRK5 vector with or without the same localization signals. After sequence verification, pLJM1 based plasmids were used in transient cDNA transfections or to produce lentivirus needed to generate cell lines stably expressing these proteins. pRK5 based plasmids were also used for transient transfection experiments. The p18<sup>mito</sup> expression plasmid was generated by cloning of a mutant p18 with amino acids 2–5 changed to alanines into a modified version of the pLKO.1 vector that added, to the C terminus of p18, the mitochondrial localization signal of OMP25 protein. This plasmid was used in transient cDNA transfections or to produce lentivirus needed to generate stable cell lines. HA-Rheb1 and HA-Rheb1-HRas25 were cloned into pLJM5, a derivative of pLJM1 carrying a hygromycin instead of puromycin resistance gene. The vectors were used as above for lentivirus production.

### Immunofluorescence Assays

Fifty thousand HEK293T cells or 20,000 of other cell types were plated on fibronectin-coated glass coverslips in 12-well tissue culture plates. Twenty-four hours later, the slides were rinsed with PBS once and fixed for 15 min with 4% paraformaldehyde in PBS warmed to 37°C. The slides were rinsed

(H) Model for amino-acid induced mTORC1 activation. In the absence of amino acids, mTORC1 cannot associate with the endomembrane system and has no access to its activator Rheb. In the presence of amino acids, the Rag GTPases, which are tethered to the lysosomal surface by the Ragulator, serve as a docking site for mTORC1, allowing mTORC1 to associate with endomembranes and thus encounter and become activated by Rheb.

See also Figure S5.

twice with PBS and cells were permeabilized with 0.05% Triton X-100 in PBS for 30 s. After rinsing twice with PBS, the slides were incubated with primary antibody in 5% normal donkey serum for 2 hr at room temperature, rinsed four times with PBS, and incubated with secondary antibodies produced in donkey (diluted 1:1000 in 5% normal donkey serum) for 1 hr at room temperature in the dark, washed four times with PBS. Slides were mounted on glass coverslips using Vectashield (Vector Laboratories) and imaged. Transient transfections for immunofluorescence assays were performed as described in the [Extended Experimental Procedures](#).

## SUPPLEMENTAL INFORMATION

Supplemental Information includes Extended Experimental Procedures and Five Figures and can be found with this article online at [doi:10.1016/j.cell.2010.02.024](https://doi.org/10.1016/j.cell.2010.02.024).

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## EXTENDED EXPERIMENTAL PROCEDURES

### Materials

Reagents were obtained from the following sources: antibodies to phospho-T389 S6K1, S6K1, mTOR, raptor, RagA/B, RagC, p14, p18, MP1, the myc epitope, the HA epitope, the FLAG epitope (unconjugated and alexa fluor conjugated), TSC2, phospho-T398 dS6K, phospho-S473 Akt, Akt1, phospho-T70 4E-BP1, 4E-BP1, and Rheb from Cell Signaling Technology; antibodies to LAMP2 from Abcam (ab25631 and ab13524); antibody to raptor (for immunostaining) from Millipore; antibody to Cytochrome c from BD Biosciences; HRP-labeled anti-mouse, anti-goat, and anti-rabbit secondary antibodies from Santa Cruz Biotechnology; FLAG M2 affinity gel, FLAG M2 antibody, human recombinant insulin, from Sigma Aldrich; protein G-sepharose and dialysis cassettes from Thermo Scientific; DMEM from SAFC Biosciences; FuGENE 6 and Complete Protease Cocktail from Roche; alexa fluor conjugated secondary antibodies from Invitrogen; 16% paraformaldehyde solution from Electron Microscopy Sciences; fibronectin from Jackson ImmunoResearch Laboratories; 35 mm glass bottom dishes from Mattek Corporation; glass coverslips from Ted Pella, Inc; amino acid and glucose-free RPMI from United States Biological; Schneider's medium, *Drosophila*-SFM, and Inactivated Fetal Calf Serum (IFS) from Invitrogen. The dS6K antibody was a generous gift from Mary Stewart (North Dakota State University).

### Preparation of Cell Lysates and Immunoprecipitations

Cells were rinsed once with ice-cold PBS and lysed in ice-cold lysis buffer (40 mM HEPES [pH 7.4], 2 mM EDTA or 5mM MgCl<sub>2</sub>, 10 mM pyrophosphate, 10 mM glycerophosphate, 0.3% CHAPS, or 1% Triton X-100 and one tablet of EDTA-free protease inhibitors (Roche) per 25 ml). The soluble fractions of cell lysates were isolated by centrifugation at 13,000 rpm for 10 min by centrifugation. For immunoprecipitations, primary antibodies were added to the lysates and incubated with rotation for 1.5 hr at 4°C. 60 µl of a 50% slurry of protein G-sepharose was then added and the incubation continued for an additional 1 hr. Immunoprecipitates were washed three times with lysis buffer containing 150mM NaCl. Immunoprecipitated proteins were denatured by the addition of 20 µl of sample buffer and boiling for 5 min, resolved by 8%–16% SDS-PAGE, and analyzed by immunoblotting. For Flag purifications, Flag M2 affinity gel was washed with lysis buffer 3 times. 20 µl of beads in 50% slurry was then added to pre-cleared cell lysates and incubated with rotation for 2 hr at 4°C. Finally, The beads were washed 3 times with lysis buffer containing 150 mM NaCl. Immunoprecipitated proteins were denatured by the addition of 50 µl of sample buffer and boiling for 5 min.

### Mammalian Lentiviral shRNAs and cDNAs

The sequences of shRNAs targeting human MP1 and p18 are as follows:

MP1\_1: GAGATGGAGTACCTGTTATTA  
MP1\_2: ATATCAATCCAGCAATCTTTA  
p18: AGACAGCCAGCAACATCATTG

### Identification of Regulator Components as Rag-Associated Proteins

Regulator components (MP1, p14, and p18) were detected in anti-FLAG immunoprecipitates prepared from HEK293T cells stably expressing FLAG-RagB or FLAG-RagD as well as in immunoprecipitates of endogenous RagC prepared from HEK293T cells. Immunoprecipitates were prepared as described (Sancak et al., 2008). Proteins were eluted with the FLAG peptide from the anti-FLAG affinity matrix or recovered from the protein G-sepharose by boiling with sample buffer, resolved by SDS-PAGE, and stained with simply blue stain (Invitrogen). Each gel lane was sliced into 10–12 pieces and the proteins in each gel slice digested overnight with trypsin. The resulting digests were analyzed by mass spectrometry as described (Sancak et al., 2008). 2–3 peptides corresponding to each Regulator component were identified in the FLAG-RagB and endogenous RagC immunoprecipitates, while no peptides corresponding to any of the proteins were ever found in the FLAG-Rap2a, p53, or  $\alpha$ -tubulin immunoprecipitates that served as controls.

### Amino Acid Starvation and Stimulation and dsRNA-Mediated Knockdowns in *Drosophila* Cells

Amino acid starvation and stimulation of *Drosophila* S2 cells was performed as described (Sancak et al., 2008). The design and synthesis of dsRNAs has also been described (Sancak et al., 2008).

Primer sequences used to amplify DNA templates for dsRNA synthesis for dp14, dp18, and dMP1, including underlined 5' and 3' T7 promoter sequences, are as follows:

dp14 (CG5189) dsRNA forward primer: GAATTAATACGACTCACTATAGGGAGACTCTATTGGCCTACTCCGTTAT  
dp14 (CG5189) dsRNA reverse primer: GAATTAATACGACTCACTATAGGGAGATATGAGCCGAGATCTGCTTA  
dp18 (CG14184) dsRNA forward primer: GAATTAATACGACTCACTATAGGGAGAGCAGAATACTGCGATAAACATGATA  
dp18 (CG14184) dsRNA reverse primer: GAATTAATACGACTCACTATAGGGAGATGGATAGGTTGGCTTAGACAGATAG  
dMP1 (CG5110) dsRNA forward primer: GAATTAATACGACTCACTATAGGGAGAGTCGACGACATCAAGAAGTATTTA  
dMP1 (CG5110) dsRNA reverse primer: GAATTAATACGACTCACTATAGGGAGAGTACATGGAGATGATGGTCTTGT

### In Vitro Binding Assay

2 million HEK293T cells were transfected with 2  $\mu$ g FLAG-p18 (lipidation mutant G2A), 2  $\mu$ g HA-GST-Rap2a, or 2  $\mu$ g HA-GST-RagB together with 2  $\mu$ g of HA-GST-RagC. 2 days after transfection, the cells were lysed in lysis buffer containing 1% Triton X-100 as described (Sancak et al., 2007) and cleared lysates were incubated with glutathione- or FLAG-beads for 3 hr at 4°C with rotation. The beads were washed 3 times with lysis buffer and two times with lysis buffer containing 0.3% CHAPS. FLAG-p18 was eluted from FLAG beads with the FLAG peptide and 1/8 of the eluate was incubated with 1/4 of the Rag-containing glutathione beads in lysis buffer with 0.3% CHAPS for 45 min at 4°C. The glutathione beads were washed three times with lysis buffer containing 0.3% CHAPS and 150 mM NaCl. Proteins were denatured by the addition of 20  $\mu$ l of sample buffer and boiling for 5 min and analyzed by SDS-PAGE and immunoblotting.

### Transient Transfections for Immunofluorescence Assays

For myc-mTOR and HA-raptor co-transfection experiments, HEK293T cells were seeded in 60 mm culture plates. 24 hr later, cells were transfected with 500 ng myc-mTOR and 50 ng HA-Raptor. 24 hr after transfections, cells were split and plated on fibronectin coated glass coverslip in 12-well culture plates and processed as above.

For GFP-RagB, GFP-RagD, p18-GFP, GFP-Mito, RFP-RagB, and LAMP1-mRFP co-transfection experiments, HEK293T cells (250,000 cells/dish) or p18<sup>-/-</sup>, p18<sup>rev</sup> or p18<sup>mito</sup> cells (50,000 cells/dish) were plated on 35 mm, glass-bottom Mattek dishes. The next day, each dish was transfected with 100 ng of GFP-RagB or GFP-RagD, p18-GFP, GFP-mito, RFP-RagB or LAMP1-mRFP using fugene. At 18–24 hr post transfections, cells were fixed and imaged. GFP-Mito has been described (Nemoto and De Camilli, 1999).

For GFP-LC3 localization experiments, 2 million cells were transfected by electroporation with 1  $\mu$ g of GFP-LC3 plasmid, and plated on 35 mm glass-bottom Mattek dishes. The next day the cells were starved for 3 hr in serum- and amino acid-free RPMI to induce autophagy and processed for imaging as above.

All images were acquired with a spinning disk confocal microscope (Perkin Elmer) equipped with a Hamamatsu 1k X 1k EM-CCD camera. For each image, 8–10 optical slices were acquired and displayed as maximum projections.

### Quantification of Number of Autophagosomes per Cell

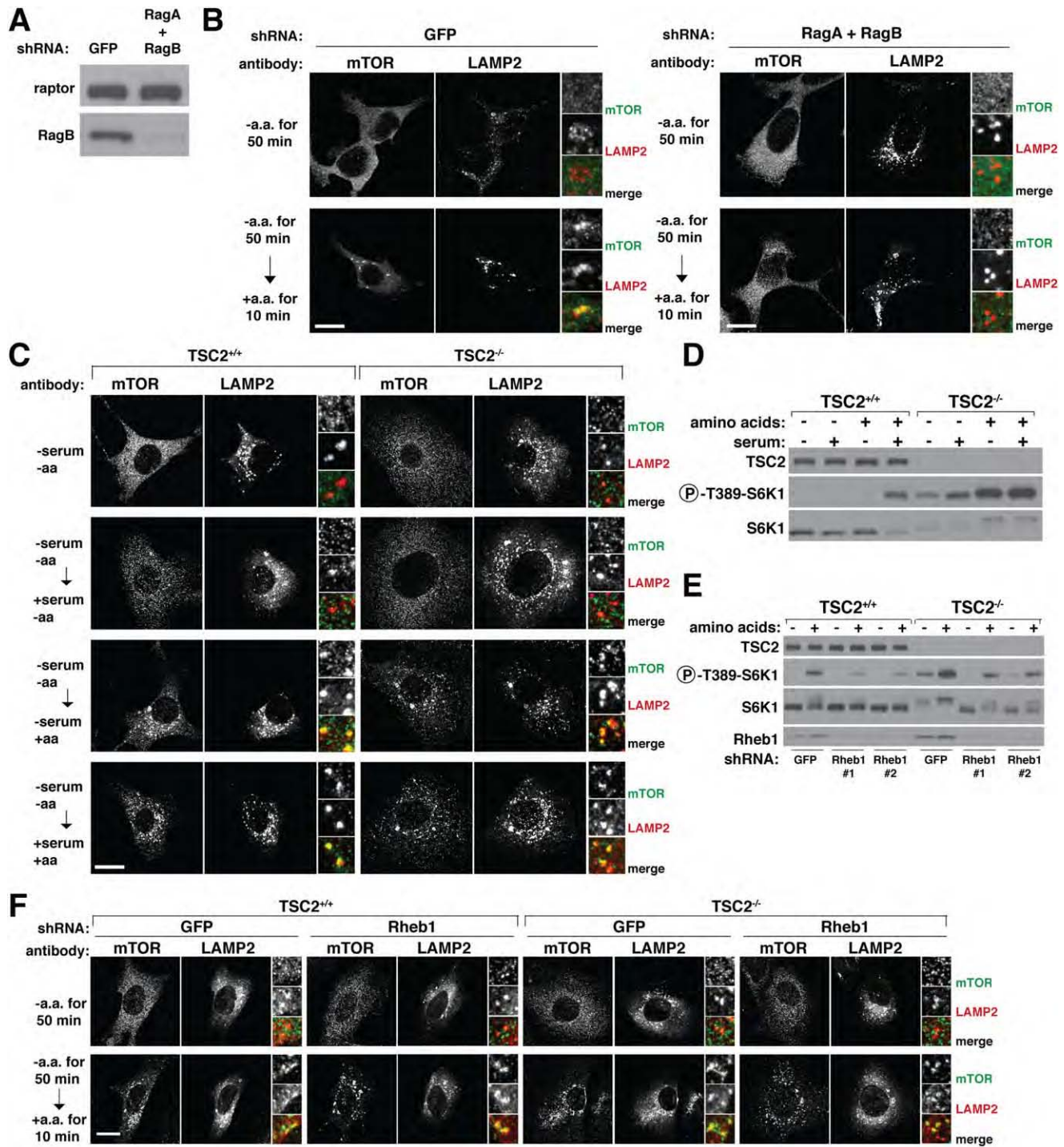
After acquisition, the images were opened with Image J, made binary and the number of autophagosomes per cell was obtained using the “Analyze Particle” function.

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**Figure S1. Movement of mTORC1 to Lysosomal Membranes in Response to Amino Acids Depends on the Rag GTPases and Is Independent of TSC1/2, Rheb, and Growth Factors, Related to Figure 1**

(A) Immunoblot analysis of RagB and raptor protein levels in HEK293T cells with an RNAi-mediated knockdown of a control protein or RagA and RagB.

(B) Images of cells with knockdowns of RagA and RagB and co-immunostained for mTOR (green) and LAMP2 (red) after starvation and restimulation with amino acids for the indicated times. HEK293T cells expressing the indicated shRNAs were starved and restimulated with amino acids as indicated and processed in the immunofluorescence assay. In all images, insets show selected fields that were magnified five times and their overlay. Scale bar is 10  $\mu$ m.

(C) mTOR co-localizes with LAMP2 only in the presence of amino acids and independently of serum stimulation. Images show co-immunostaining of mTOR (green) and LAMP2 (red) in TSC2<sup>+/+</sup> and TSC2<sup>-/-</sup> MEFs after indicated treatments. Cells were starved for serum and amino acids, and stimulated with dialyzed



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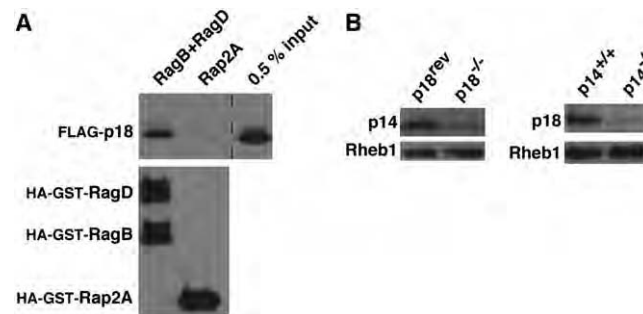
serum, amino acids, or both before processing in the immunofluorescence assay.

(D) Lysates from TSC2<sup>+/+</sup> and TSC2<sup>-/-</sup> MEFs starved and stimulated as in (A) were analyzed by immunoblotting for the activity of the mTORC1 pathway.

(E) Loss of Rheb expression inhibits mTORC1 signaling in TSC2<sup>+/+</sup> and TSC2<sup>-/-</sup> MEFs. Cells expressing the indicated shRNAs were starved for amino acids or starved and restimulated with amino acids and lysates analyzed by immunoblotting for mTORC1 pathway activity and Rheb1 levels.

(F) mTOR co-localizes with LAMP2 only in the presence of amino acids and independently of Rheb or TSC2. Images show co-immunostaining of mTOR (green) and LAMP2 (red) in TSC2<sup>+/+</sup> and TSC2<sup>-/-</sup> MEFs treated as in (C).

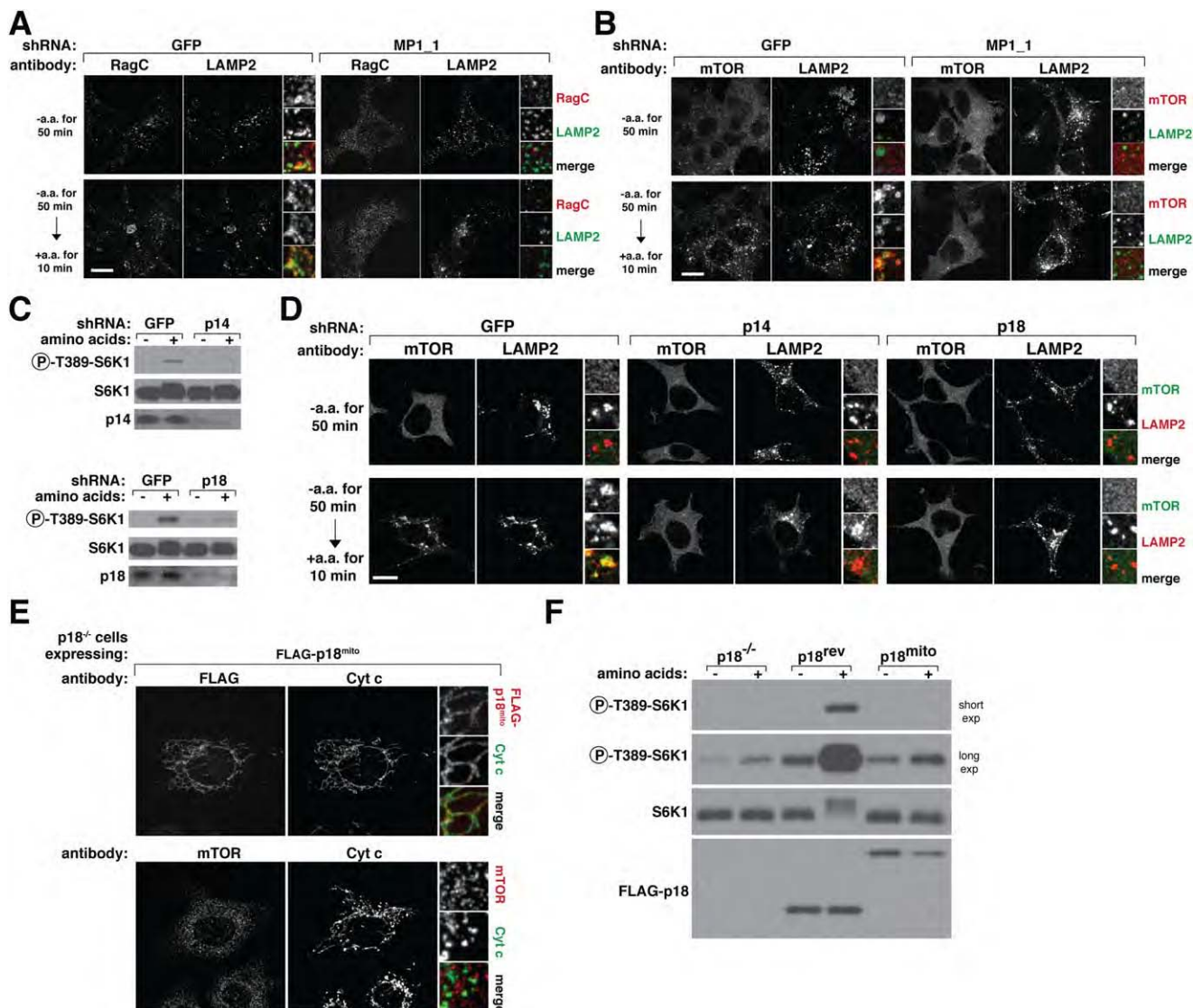
In all images, insets show selected fields that were magnified five times and their overlays. Scale bar is 10  $\mu$ m.



**Figure S2. The Expression of Regulator Proteins Is Coregulated and Purified FLAG-p18 Interacts with Purified HA-GST-RagB/HA-GST-RagD Dimer In Vitro, Related to Figure 2**

(A) In vitro binding assay using purified soluble FLAG-p18 and HA-GST-RagB/HA-GST-RagD heterodimer bound to glutathione beads was performed as described in the [Experimental Procedures](#).

(B) p14 protein levels are lower in p18 null cells than in p18 null cells expressing FLAG-p18 (p18<sup>rev</sup>). Similarly, in cells that lack p14 (p14<sup>-/-</sup>), p18 expression is reduced compared to control cells (p14<sup>+/+</sup>). Cells were grown to confluency, lysates were prepared, and the levels of the indicated proteins analyzed by immunoblotting.



**Figure S3. The Ragulator Is Required for RagC Localization to Lysosomal Membranes and Amino Acid-Induced mTOR Lysosomal Localization, Related to Figure 3**

(A) An MP1 knockdown displaces RagC from the lysosomal surface. Images of cells with shRNA-mediated knockdowns of a control protein or MP1 and co-immunostained for RagC (red) and LAMP2 (green). HEK293T cells expressing the indicated shRNAs were starved of and restimulated with amino acids for the stated times and then processed in the immunofluorescence assay.

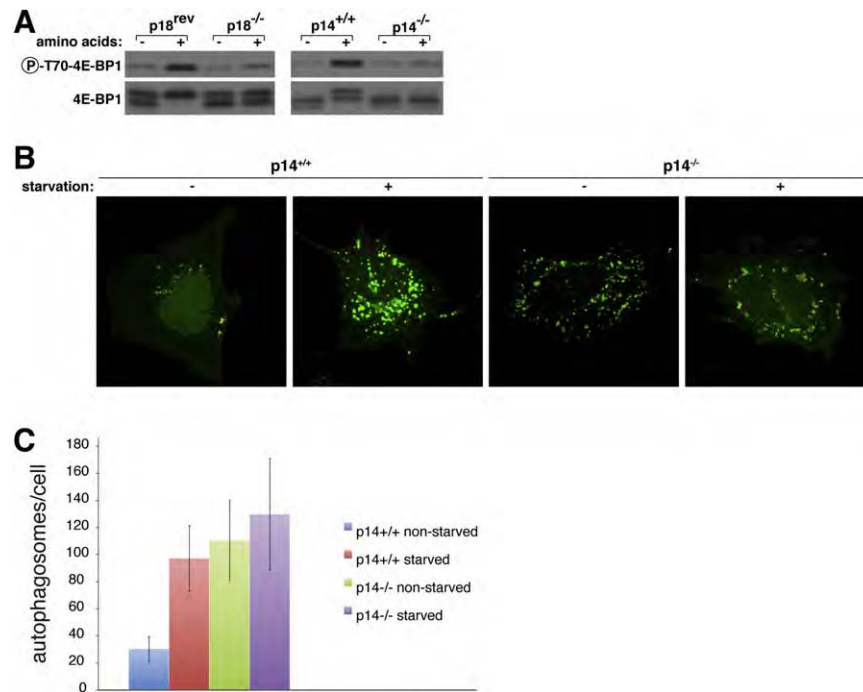
(B) An MP1 knockdown impairs the recruitment of mTOR to the lysosomal surface in response to amino acid stimulation. Images of cells with shRNA-mediated knockdowns of a control protein or MP1 and co-immunostained for mTOR (red) and LAMP2 (green). HEK293T cells expressing the indicated shRNAs were starved of and restimulated with amino acids for the stated times and then processed in the immunofluorescence assay.

(C) Knockdown of p18 or p14 in HEK293T cells impair amino acid-induced mTORC1 activation. HEK293T cells with RNAi-mediated knockdown of p14 or p18, or control cells, were starved for amino acids for 50 min or starved and restimulated with amino acid for 10 min. Cell lysates were prepared and analyzed by immunoblotting for the phosphorylation states and levels of indicated proteins.

(D) Knockdown of p18 or p14 in HEK293T cells impairs amino acid-induced lysosomal recruitment of mTOR. Control cells and cells with p14 or p18 knockdown were treated as in (C) and immunostained for mTOR (green) and LAMP2 (red). In all images, insets show selected fields that were magnified five times and their overlays. Scale bar is 10  $\mu$ m.

(E) Images of p18<sup>-/-</sup> cells stably expressing FLAG-p18<sup>mito</sup> and co-immunostained for FLAG-p18<sup>mito</sup> or mTOR (red) and Cytochrome c (Cyt c) (green).

(F) The mTORC1 pathway can be activated by amino acids in p18 null cells expressing wild-type p18 (p18<sup>rev</sup>), but not mitochondrially-targeted p18 (p18<sup>mito</sup>). Cells were starved for amino acids in the presence of dialyzed serum for 50 min, or starved and restimulated with amino acids for 10 min. Lysates were prepared and phosphorylation states and levels of indicated proteins were analyzed by immunoblotting.

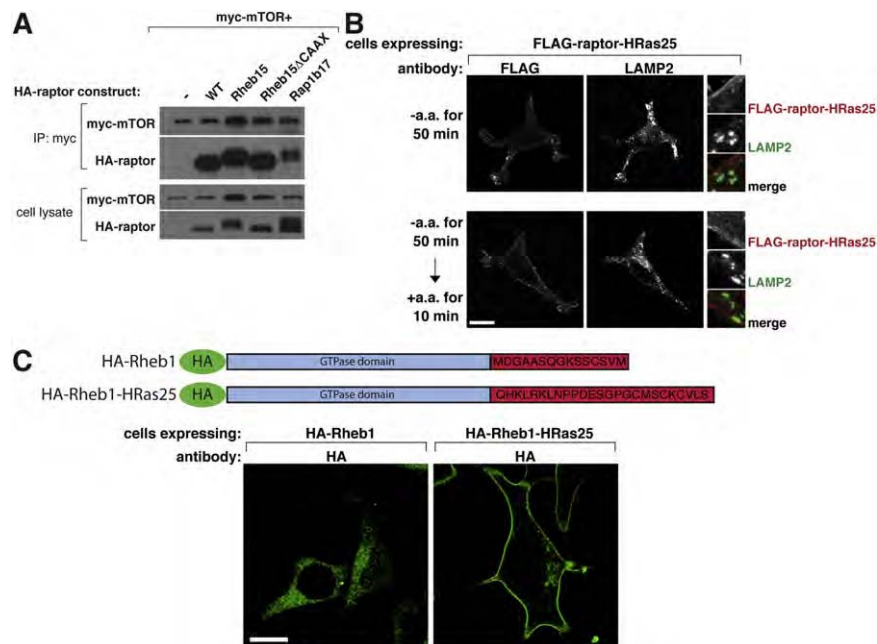


**Figure S4. 4E-BP1 Phosphorylation Is Inhibited and Autophagy Is Induced in Cells Lacking Regulator Components, Related to Figure 4**

(A) Amino acids fail to stimulate 4E-BP1 phosphorylation in cells lacking p14 or p18. Cells were starved for amino acids in the presence of dialyzed serum for 50 min, or starved and restimulated with amino acids for 10 min. Lysates were prepared and 4E-BP1 phosphorylation and levels analyzed by immunoblotting.

(B) Autophagy is induced in p14 null cells. Images of cells transiently expressing GFP-LC3 and starved for amino acids and serum for 3 hr or growing in complete media. Accumulation of GFP-LC3 in large puncta in starved control cells and in the non-starved p14 null cells indicates increased levels of autophagy in these cells.

(C) Quantification of autophagosomes in wild-type or p14 null cells expressing GFP-LC3. Cells were treated as in (B), images were taken and the number of autophagosomes per cell was quantified using Image J. At least six cells were analyzed per sample. The data are represented as mean  $\pm$  standard deviation. Starved wild-type cells, or p14 null cells, irrespective of being starved or not, show statistically significant increases in the number autophagosomes per cell compared to wild-type non-starved cells ( $p < 0.000002$ ). There is no statistically significant difference between starved and non-starved p14 null cells ( $p = 0.38$ ).



**Figure S5. Addition of Rheb1 and Rap1b Targeting Signals to Raptor Does Not Interfere with Its Binding to mTOR and Raptor-HRas25 and Rheb-HRas25 Localize to the Plasma Membrane, Related to Figure 7**

(A) HEK293T cells were co-transfected with plasmids encoding myc-mTOR and the indicated HA-raptor variants. Anti-myc immunoprecipitates as well as lysates were analyzed by immunoblotting for the indicated proteins.

(B) Raptor fused at its C terminus with the localization signal of HRas localizes to the plasma membrane. Images of cells expressing FLAG-raptor-HRas25 and starved of and restimulated with amino acid for the indicated times and co-immunostained with antibodies to the FLAG epitope (red) and endogenous LAMP2 (green).

(C) Rheb1 localizes to the plasma membrane when its localization signal is swapped for that of HRas. Schematic shows composition of the HA-Rheb1-HRas25 variant. Images of cells expressing HA-Rheb1 or HA-Rheb1-HRas25 (green).

# Structure of the Human mTOR Complex I and Its Implications for Rapamycin Inhibition

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## SUMMARY

The mammalian target of rapamycin complex 1 (mTORC1) regulates cell growth in response to the nutrient and energy status of the cell, and its deregulation is common in human cancers. Little is known about the overall architecture and subunit organization of this essential signaling complex. We have determined the three-dimensional (3D) structure of the fully assembled human mTORC1 by cryo-electron microscopy (cryo-EM). Our analyses reveal that mTORC1 is an obligate dimer with an overall rhomboid shape and a central cavity. The dimeric interfaces are formed by interlocking interactions between the mTOR and raptor subunits. Extended incubation with FKBP12-rapamycin compromises the structural integrity of mTORC1 in a stepwise manner, leading us to propose a model in which rapamycin inhibits mTORC1-mediated phosphorylation of 4E-BP1 and S6K1 through different mechanisms.

## INTRODUCTION

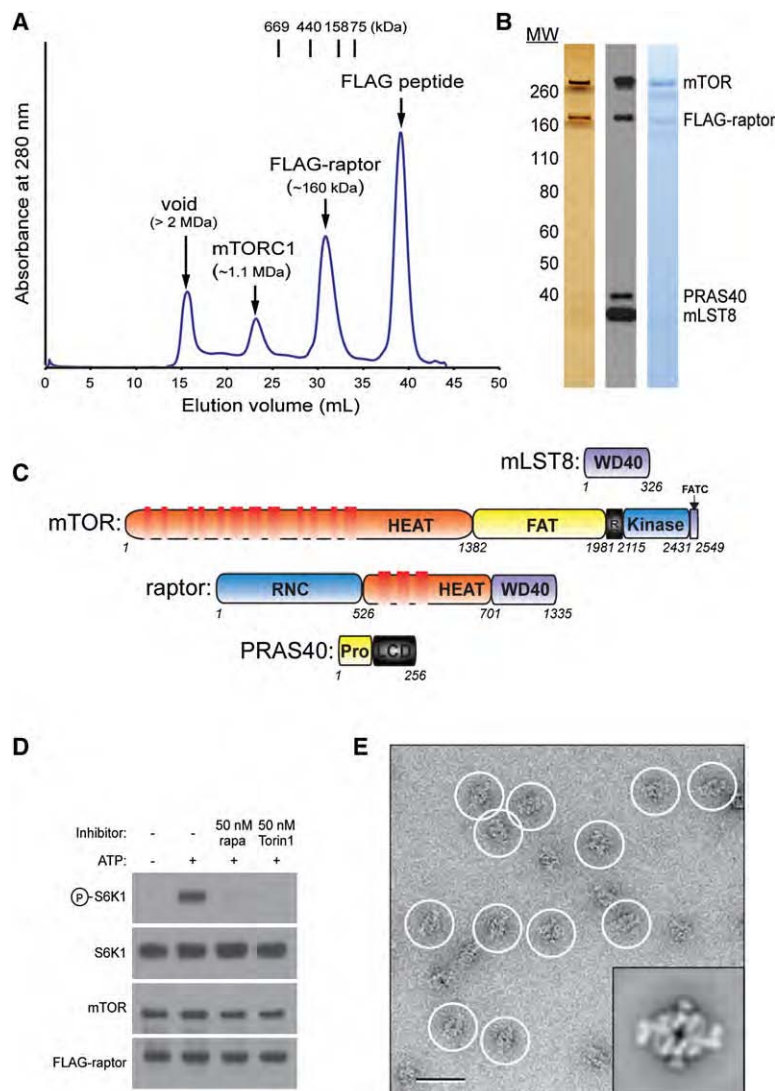
The mTOR serine/threonine kinase is a member of the phosphoinositide 3-kinase (PI3K)-related kinase (PIKK) family. This conserved protein integrates diverse upstream signals to regulate growth-related processes, including mRNA translation, ribosome biogenesis, autophagy, and metabolism (Sarbasov et al., 2005a). mTOR nucleates two large physically and functionally distinct signaling complexes: mTOR complex 1 (mTORC1) and mTOR complex 2 (mTORC2) (Guertin and Sabatini, 2007). mTORC1 consists of mTOR, raptor (regulatory associated protein of mTOR), PRAS40 (proline-rich AKT substrate 40 kDa), and mLST8 (mammalian lethal with sec-13). mTORC2, on the other hand, is composed of mTOR, mLST8, rictor (raptor independent companion of mTOR), mSIN1 (mammalian stress-activated protein kinase interacting protein 1), and Protor-1 (protein observed with rictor-1) and controls cell proliferation and survival

by phosphorylating and activating the Akt/PKB kinase (Sarbasov et al., 2005b). The key structural features that differentiate the substrate specificity of mTORC1 and mTORC2 remain unclear.

Unlike mTORC2, mTORC1 appears to play critical roles in cell growth in response to nutrients. The mTOR protein, which consists of multiple HEAT repeats at its N-terminal half followed by the FKBP12-rapamycin-binding (FRB) and serine-threonine protein kinase domains near its C-terminal end, has no known enzymatic functions besides its kinase activity. PRAS40 has been characterized as a negative regulator of mTORC1 (Sancak et al., 2007; Vander Haar et al., 2007; Wang et al., 2007), but the functions of other mTOR-interacting proteins in mTORC1 are ambiguous. Previous studies indicate that raptor may have roles in mediating mTORC1 assembly, recruiting substrates, and regulating mTORC1 activity and subcellular localization (Hara et al., 2002; Kim et al., 2002; Sancak et al., 2008). The strength of the interaction between mTOR and raptor can be modified by nutrients and other signals that regulate the mTORC1 pathway, but how this translates into regulation of the mTORC1 pathway remains elusive. The role of mLST8 in mTORC1 function is also unclear, as the chronic loss of this protein does not affect mTORC1 activity in vivo (Guertin et al., 2006). However, the loss of mLST8 can perturb the assembly of mTORC2 and its function. The small GTP-binding protein Rheb (Ras homolog enriched in brain) binds near the mTOR kinase domain (Long et al., 2005) and seems to have a key role in stimulating the kinase activity of mTORC1 (Long et al., 2005; Sancak et al., 2007).

mTORC1 can be hyperactivated by oncogenic phosphoinositide 3-kinase signaling and promotes cellular growth in cancer (Guertin and Sabatini, 2007; Shaw and Cantley, 2006). mTORC1 drives growth through at least two downstream substrates, S6 kinase 1 (S6K1) and eIF-4E-binding protein 1 (4E-BP1) (Richter and Sonenberg, 2005; Ma and Blenis, 2009). The regulation of the activity of mTORC1 toward these and yet unidentified substrates appears to be complex and is likely to be dependent on the organization of the various subunits in the mTORC1 complex. The study of mTORC1 phosphorylation of substrate sites has been greatly aided by pharmacological inhibitors of mTORC1, in particular rapamycin. Rapamycin, in complex with its intracellular receptor FKBP12 (FK506-binding protein of



**Figure 1. mTORC1 Purification**

(A) mTORC1 and FLAG-raptor were purified by tandem gel filtration chromatography. Their masses were estimated based on known molecular weight standards as indicated (Thyroglobulin [669 kDa], Ferritin [440 kDa], Aldolase [158 kDa], and Conalbumin [75 kDa]).

(B) The gel filtration fraction corresponding to mTORC1 was analyzed by SDS-PAGE followed by silver and Coomassie staining as well as immunoblotting for indicated proteins.

(C) Schematics of mTORC1 components illustrating the various predicted domains.

(D) In vitro kinase assay showing that purified mTORC1 phosphorylates S6K1 and is inhibited by both rapamycin-FKBP12 (rapa) and Torin1.

(E) EM of negatively stained mTORC1. A raw image of mTORC1 particles (circled) and a representative class average from the classification of 10,080 particles (inset). The scale bar represents 50 nm, and the side length of the panel showing the class average is 45 nm.

See also Figure S1.

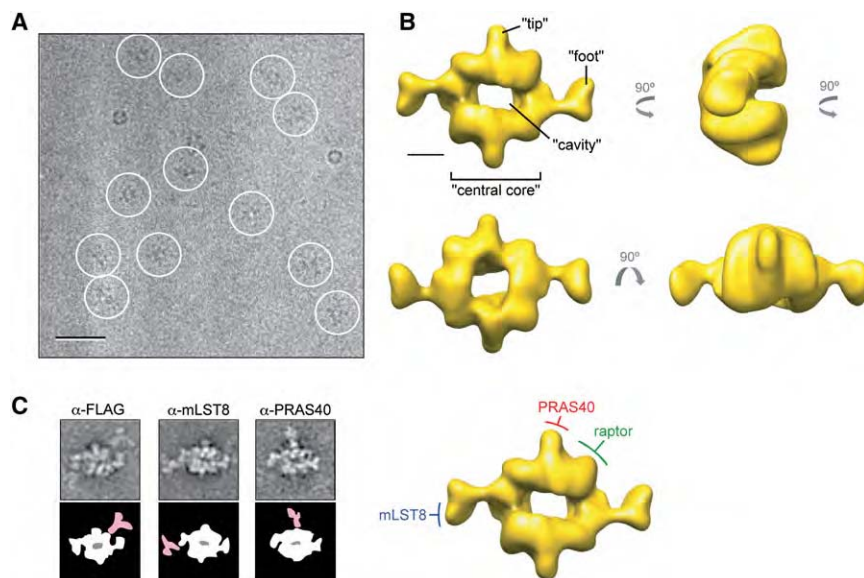
## RESULTS AND DISCUSSION

### Purification of Human mTORC1

The large size (~1 MDa) and instability of mTORC1 make it difficult to obtain the purified complex for structural analysis. To address this issue, we devised a method to purify microgram quantities of intact and active human mTORC1. Keys to the successful purification of mTORC1 were (1) the development of a human cell line stably expressing a tagged raptor subunit that incorporates into endogenous mTORC1, (2) the identification of buffer conditions that minimize mTORC1 disintegration and/or aggregation during purification, and (3) the implementation of tandem gel filtration chromatography steps to separate mTORC1 from other large contaminants (Figure 1A). Purified mTORC1 consists of equimolar quantities of mTOR, raptor, and mLST8 and of PRAS40 at sub-

stoichiometric level (Figures 1B and 1C). The kinase activity of purified mTORC1 toward S6K1 was sensitive to FKBP12-rapamycin and Torin1, an ATP-competitive inhibitor of mTOR (Thoreen et al., 2009) (Figure 1D). Negative-stain EM analysis of the purified complex revealed particles that were homogeneous in size and shape (Figure 1E). Projection averages calculated from the classification of 10,080 particle images illustrated that mTORC1 has an elongated, rhomboid shape with a central, stain-filled cavity and "feet-like" protrusions emanating from both ends of the molecule (Figure 1E, inset, and Figure S1 available online). The averages displayed a 2-fold symmetry. This observation, together with the mass estimated from gel filtration, provides evidence for the obligate dimeric organization of mTORC1 that had been previously suggested by genetic and coimmunoprecipitation studies (Zhang et al., 2006; Takahara et al., 2006; Urano et al., 2007; Wang et al., 2006). Although PRAS40 was present in substoichiometric amounts in our purified mTORC1 sample, the fact that all averages show particles

12 kDa), acutely inhibits mTORC1 by binding to the FRB domain of mTOR (Sarbasov et al., 2005a). Yet, the molecular mechanism of how this high-affinity interaction perturbs mTOR kinase activity and the fully assembled mTORC1 is currently unknown. Although there have been attempts to model the N-terminal domain of mTOR based on the low-resolution structure of human DNA-PK (Sibanda et al., 2010), these efforts have failed to provide insights into the function and regulation of the mTOR kinase. Thus, a detailed knowledge of mTORC1 structure, including the organization of its components, has the potential to help understand the regulation of its kinase activity and to aid in the development of more effective mTORC1 inhibitors. We report the three-dimensional (3D) structure of human mTORC1 as determined by cryo-EM. This structure, together with labeling and biochemical studies, reveals the intricate organization of the components within mTORC1 and provides structural insights into the mechanism of its inhibition by FKBP12-rapamycin.



**Figure 2. Cryo-EM Reconstruction of mTORC1 and Its Molecular Organization**

(A) Image of a vitrified specimen showing individual mTORC1 particles (circled). The scale bar represents 50 nm.

(B) Different views of the 3D reconstruction of mTORC1 filtered to 26 Å, with the main structural features denoted. The scale bar represents 5 nm.

(C) Molecular organization of mTORC1. (Left) Representative class averages from antibody labeling experiments of mTORC1 (top) and schematic representations showing mTORC1 in white and the antibody in pale red (bottom). The side length of each panel is 45 nm. (Right) Location of raptor, mLST8, and PRAS40 in the cryo-EM density map of mTORC1.

See also Figure S2.

with identical overall shape suggests that PRAS40 contributes little to the density of the complex and is not required for proper assembly and stability of mTORC1. Our projection structure does not resemble the monomeric structure obtained from the recent negative-stain EM analysis of *Saccharomyces cerevisiae* TOR in complex with KOG1 (the raptor homolog in yeast) (Adami et al., 2007). These striking differences may be due to the differences in composition and stoichiometry of known components within the two TOR complexes. The sample used in the EM study of the yeast complex may not reflect a fully assembled TORC1 complex but, rather, a subassembly. For example, LST8, a bona fide yeast TORC1 component, is missing in the analyzed sample of the yeast study. In addition, human mTOR and raptor are only conserved over limited regions compared to their yeast orthologs, TOR1 and KOG1, respectively. Therefore, it is conceivable that human mTORC1 and yeast TORC1 could adopt different quaternary structures.

### Cryo-EM Structure of mTORC1

To determine the 3D structure of mTORC1 by cryo-EM, we first produced a reliable initial model by calculating a random conical tilt (RCT) reconstruction with 50°/0° tilt pair images of cryo-negatively stained specimens (Figure S2). Collecting images of vitrified mTORC1 specimens proved difficult due to low protein concentration (attempts to concentrate mTORC1 samples were unsuccessful) and a strong tendency of mTORC1 to dissociate upon contact with the air-water interface. We overcame these difficulties by adsorbing mTORC1 to a thin carbon film prior to vitrification. Even so, only a few particles were present (Figure 2A), requiring us to collect many images to obtain a sufficient number of particles for structure determination. The carbon film also induced mTORC1 to adsorb to the grid in a preferred orientation, making it necessary to collect images of tilted specimens to obtain the multiple views needed for 3D reconstruction. The final data set contained 28,325 particle images, including 3,905 from 45° tilted specimens. A 3D recon-

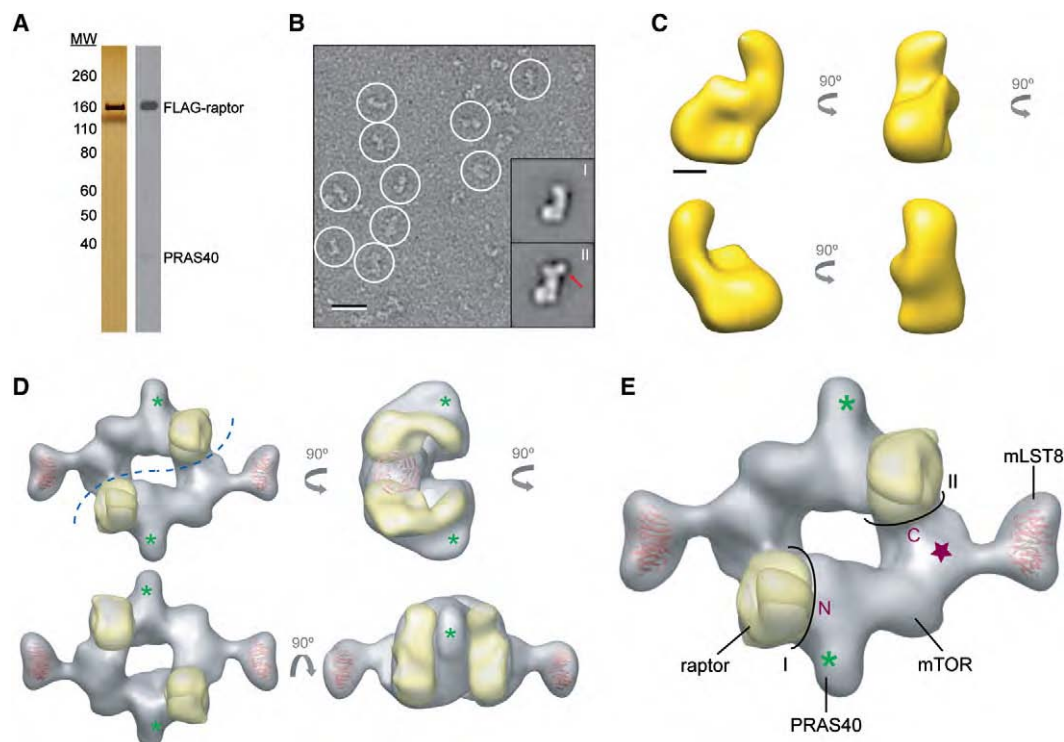
struction was calculated by aligning these individual images of the vitrified complex to the initial model produced with the cryo-negatively stained sample, followed by iterative refinement of their orientation parameters. The estimated resolution of the final reconstruction is 26 Å according to the Fourier shell correlation = 0.5 criterion (Figure S2). However, the resolution is clearly anisotropic, with lower resolution in the direction perpendicular to the carbon film, a result of the limited number of views other than the face-on view (Figure S2). mTORC1 has overall dimensions of  $\sim 290 \text{ Å} \times 210 \text{ Å} \times 135 \text{ Å}$  and an estimated volume of  $1.4 \times 10^6 \text{ Å}^3$  at the contour level of the displayed map, which was chosen to be consistent with the calculated molecular mass of dimeric mTORC1 (Figure 2B).

The cryo-EM structure reveals a central cavity that has an oval shape when viewed from one face but a rectangular shape from the opposite face, with two troughs located at the extensions linking the central core to the “feet-like” structures. Though the biological relevance of this cavity remains elusive, its location between the two “monomeric” complexes may enable substrates with multiple phosphorylation sites, such as 4E-BP1 (Gingras et al., 1999), to shuttle between the two mTOR active sites within the complex. Another, albeit less likely, possibility is that the cavity may serve as a docking platform for nucleic acids because its size ( $\sim 40 \text{ Å} \times 28 \text{ Å}$ ) is large enough to accommodate double-stranded DNA (dsDNA). Though mTORC1 has not yet been shown to interact with dsDNA or other macromolecules, several members of the PIKK family (Keith and Schreiber, 1995), most notably DNA-PK, are known to mediate DNA repair by directly binding to DNA (Gottlieb and Jackson, 1993; Spagnolo et al., 2006).

### Subunit Organization of mTORC1 and EM Structure of Raptor

Whereas the cryo-EM structure revealed the overall shape of mTORC1, at the current resolution, it was not possible to define intermolecular and intersubunit boundaries. Therefore,





**Figure 3. Three-Dimensional Reconstruction of Raptor and Molecular Docking**

(A) Silver-stained gel and immunoblot of the gel filtration fraction containing free raptor detected the presence of PRAS40.

(B) EM image of negatively stained raptor (circled) and two representative class averages from the classification of 12,216 particles (bottom-right insets). Class II particles contain an additional density (red arrow) compared to class I particles, which likely represents PRAS40. The scale bar represents 25 nm, and the side length of the panels showing the class averages is 27 nm.

(C) Different views of the raptor 3D reconstruction. The scale bar represents 2.5 nm.

(D) Two copies of the raptor 3D reconstruction (gold) and two models of a representative WD40 domain (PDB code 3EMH, red) were placed into the cryo-EM density map (gray). The green asterisk depicts the location of PRAS40 as determined by antibody labeling. The blue dotted line represents the dimer interface.

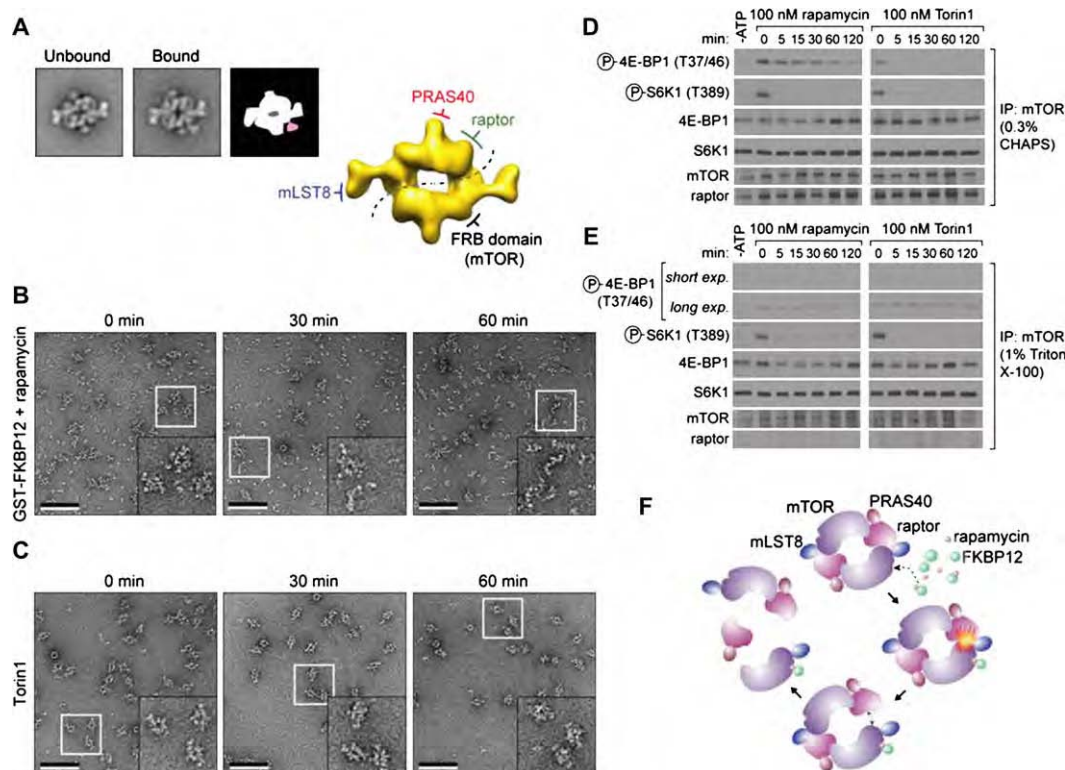
(E) The proposed locations of the N- and C-terminal domains (marked "N" and "C") and the kinase domain of mTOR (purple star). The black lines labeled "I" and "II" delineate the two interaction interfaces formed by each mTOR molecule with the two raptor subunits.

See also Figure S3.

we performed antibody labeling experiments to localize individual subunits within mTORC1, including raptor (detected through its FLAG tag), mLST8, and PRAS40. The labeled particles were imaged by negative-stain EM and analyzed by classification and image averaging. We discovered that mLST8 localizes to the distal foot-like structures, PRAS40 to the small tips in the midsection of the central core, and the N terminus of raptor to the corner of the core (Figure 2C). The occasional observation of double-labeled particles provided further assurance for the dimeric organization of mTORC1 (Figure S2).

In addition, we determined the EM structure of raptor. FLAG-tagged raptor that did not incorporate into mTORC1 eluted as a separate peak from gel filtration (Figures 1A and 3A). Purified raptor was homogeneous in size and shape according to negative-stain EM analysis (Figures 3B and S3). The 3D reconstruction of raptor, determined by the RCT approach using 60°/0° image pairs of negatively stained specimens (Figure S3), revealed that its overall shape resembles a "comma" with the circular lobe likely representing the predicted C-terminal WD40 domain (Kim et al., 2002) (Figure 3C). Utilizing the antibody labeling data as a guide, the structure of mTORC1 provides an adequate frame-

work in which the EM reconstruction of raptor can be meaningfully fitted (gold surface in Figure 3D). Because mLST8 is solely composed of a seven-bladed  $\beta$ -propeller (Kim et al., 2003), we next docked two  $\beta$ -propeller models (PDB code 3EMH) into the "foot" substructures (Figure 3D). By subtracting two copies of raptor and mLST8, the densities occupied by two mTOR subunits can be predicted while accounting for minor contributions by the two small PRAS40 subunits (Figure 3D). It has been shown that the C-terminal kinase domain of mTOR associates with mLST8 (Kim et al., 2003), suggesting that this domain is likely positioned adjacent to the "foot" (purple star in Figure 3E). From the position of the kinase domain, we deduced that the N terminus of mTOR interacts with the flat face of one raptor molecule (bottom-left view in Figure 3C), forming interface I, whereas the C terminus interacts with the side of the second raptor molecule (top-right view in Figure 3C), forming interface II. The interlocking raptor-mTOR interactions within the central core provide an understanding of the basis of dimerization and illustrate the crucial function of raptor in mediating and maintaining the higher-order organization of mTORC1 (Figure 3E). In contrast, each mLST8 contacts only one mTOR within the complex. Its localization to



**Figure 4. Effects of Rapamycin-FKBP12 on mTORC1**

(A) Representative class averages of untreated mTORC1 (left) and mTORC1 treated with 50 nM of rapamycin and 0.02  $\mu\text{g}/\mu\text{l}$  GST-FKBP12 (middle) and a schematic representation showing the additional density in pale red (right). The side length of each panel is 45 nm. To the right, the location of the FRB domain with respect to the other components in the cryo-EM map of mTORC1 is shown.

(B and C) Purified mTORC1 was treated with 50 nM of rapamycin and 0.02  $\mu\text{g}/\mu\text{l}$  GST-FKBP12 or 100 nM Torin1. EM images of negatively stained samples were taken at the indicated time points. The inset in each image shows an enlarged view of the area marked by the white square. The scale bars represent 100 nm. (D and E) mTOR immunoprecipitates, prepared in lysis buffers containing 0.3% CHAPS or 1% Triton X-100, were subjected to in vitro kinase assays using 4E-BP1 or S6K1 as a substrate in the presence of 100 nM rapamycin and 0.02  $\mu\text{g}/\mu\text{l}$  FKBP12 or 100 nM Torin1. Assays were then analyzed by immunoblotting for the indicated proteins and phosphorylation states.

(F) A model depicting a potential mechanism of mTORC1 inhibition by FKBP12-rapamycin.

See also Figure S4.

the distal “foot” structures suggests that it could potentially assist substrate entry into the catalytic site.

According to our data and composite model, PRAS40 localizes in close proximity to raptor (asterisk in Figure 3D), which is in agreement with the known binding of PRAS40 to raptor (Sancak et al., 2007; Wang et al., 2007). Of interest, some class averages of purified raptor showed an additional small density, which may represent bound PRAS40 (indicated by red arrow in Figures 3B and S3). This interpretation is supported by immunoblots that show PRAS40 to be present in the analyzed raptor fraction (Figure 3A). Thus, our structural data suggest that PRAS40 inhibition is not likely to be achieved through an interaction of PRAS40 with the mTOR kinase domain. Instead, it favors the model that PRAS40 acts as a competitive inhibitor for the binding of mTORC1 substrates to raptor (Wang et al., 2007).

#### FKBP12-Rapamycin Destabilizes mTORC1 in a Stepwise Manner

With a more detailed understanding of the subunit organization of mTORC1, we next investigated how rapamycin affects its

structure. As an allosteric inhibitor of mTORC1, rapamycin requires the intracellular protein FKBP12 to form a gain-of-function complex, which directly interacts with the FKBP12-rapamycin-binding (FRB) domain of mTOR (Chen et al., 1995; Sabatini et al., 1994). The crystal structure of FKBP12-rapamycin in complex with the FRB domain did not reveal how this interaction prevents phosphorylation of direct mTORC1 substrates (Choi et al., 1996). Previous biochemical studies indicated that binding of FKBP12-rapamycin to mTORC1 induces a conformational change that weakens the mTOR-raptor interaction (Kim et al., 2002). To test this hypothesis, we incubated mTORC1 with N-terminal GST-tagged FKBP12 in the presence of 50 nM rapamycin for 15 min and then visualized the particles by negative-stain EM (Figure S4). Although the raw images did not reveal any obvious structural changes (Figure S4), image classification showed that about 10% of the particles featured an additional density, likely constituting FKBP12-rapamycin, tethered to the region that we assigned to mTOR and directly opposite of raptor (Figure 4A). Of interest, we did not observe individual particles or averages of mTORC1 showing two extra densities, suggesting

that either mTORC1 cannot accommodate two FKBP12-rapamycin complexes or that this intermediate is short lived.

Whereas relatively short exposure to FKBP12-rapamycin did not affect the structural integrity of mTORC1, extended incubations resulted in a drastic reduction in the total number of intact mTORC1 particles. Many smaller fragments appeared in the background, suggesting that FKBP12-rapamycin may cause disassembly of mTORC1 (Figure 4B). Once initiated, this dissociation appears to be swift, as we were unable to detect intermediates with defined structures during the course of the reaction (data not shown). After 1 hr incubation, virtually no intact mTORC1 particles could be detected, and the sample contained only smaller fragments, likely representing free mTOR or its subcomplexes, and undefined aggregates (Figure 4B). In contrast, Torin1 did not affect mTORC1 stability even after extended incubation (Figure 4C).

The disruption of mTORC1 by FKBP12-rapamycin may play a role in the inhibition by rapamycin of mTORC1 kinase activity toward certain substrates. Consistent with the time-dependent effects of FKBP12-rapamycin on the structural integrity of mTORC1, FKBP12-rapamycin significantly inhibited the *in vitro* phosphorylation of 4E-BP1 by mTORC1 only after mTORC1 had been incubated with the drug for at least 60 min (Figure 4D). In contrast, FKBP12-rapamycin rapidly blocked the phosphorylation of S6K1 by mTORC1, and Torin1 quickly blocked the phosphorylation of both S6K1 and 4E-BP1. In close agreement with *in vitro* kinase assays, *in vivo* experiments produced similar time-dependent effects of rapamycin on endogenous 4E-BP1, but not S6K1 (Figure S4). To assess the importance of mTORC1 integrity in the phosphorylation of S6K1 and 4E-BP1, we prepared mTORC1 that lacked raptor (Kim et al., 2002). Though raptor-free mTORC1, as predicted (Hara et al., 2002), could not support 4E-BP1 phosphorylation, it was capable of phosphorylating full-length S6K1 (Figure 4E). Furthermore, the phosphorylation of S6K1 by raptor-free mTORC1 was still inhibited by FKBP12-rapamycin. Thus, contrary to previous assumptions, raptor is dispensable for mTORC1 to phosphorylate S6K1 in a rapamycin-sensitive fashion *in vitro*. Our results suggest an important role for the mTORC1 dimer in 4E-BP1 phosphorylation. Perhaps, 4E-BP1 binds to the raptor in one monomer but is phosphorylated by the kinase of the adjacent monomer, such that, in the absence of dimerization, 4E-BP1 is not in a position to be phosphorylated.

Based on these observations and our knowledge of the molecular organization of mTORC1, we propose the following model for rapamycin-mediated inhibition of mTORC1. The initial binding of one FKBP12-rapamycin to mTORC1 causes a subtle conformational change in mTOR that weakens the mTOR-raptor interaction but does not suffice to disrupt the dimeric architecture. Moreover, the bound FKBP12-rapamycin likely occludes the binding of or blocks access to the active site for larger-sized substrates, such as S6K1. Over time, either amplified structural strain caused by the first FKBP12-rapamycin or, perhaps, the binding of a second rapamycin complex leads to a fast disintegration of the already “weakened” mTORC1 and the complete abolishment of 4E-BP1 phosphorylation (Figure 4F). Therefore, our work suggests that *in vitro* rapamycin is an mTORC1 inhibitor that may work through at least two different modes. The fact

that, within cells, rapamycin does not completely inhibit 4E-BP1 phosphorylation (Choo et al., 2008; Thoreen et al., 2009; Feldman et al., 2009) or mTORC1 stability (Kim et al., 2002) suggests that cells contain buffering mechanisms that counter the effects of rapamycin on mTORC1 and that these are lost when mTORC1 is purified.

## EXPERIMENTAL PROCEDURES

### Protein Expression and Purification

mTORC1 was purified from a HEK293T cell line that stably expresses N terminally FLAG-tagged raptor by FLAG-M2 monoclonal antibody-agarose and gel filtration. Details of the expression method and purification conditions are described in the Supplemental Experimental Procedures.

### In Vitro Kinase Assay

Kinase assays were performed using immunoprecipitated mTORC1 and inactive 4E-BP1 or S6K1 as a substrate. Reactions were analyzed by SDS-PAGE and immunoblotting. Details of the assay conditions are described in the Supplemental Experimental Procedures.

### Electron Microscopy

Negatively stained specimens were prepared as described (Ohi et al., 2004). Images were collected with a Tecnai T12 electron microscope (FEI) equipped with a LaB<sub>6</sub> filament and operated at an acceleration voltage of 120 kV. Images were recorded on imaging plates at a nominal magnification of 67,000 using a defocus value of  $\sim 1.5$   $\mu$ m. Cryo-negatively stained specimens were prepared as described (Ohi et al., 2004). Grids used to collect image pairs of 50°/0° tilted specimens were loaded on an Oxford cryo-transfer holder. Images were taken under low-dose conditions at a nominal magnification of 50,000 $\times$  and a defocus value of  $\sim 2.5$   $\mu$ m using a Tecnai F20 electron microscope (FEI) equipped with a field emission electron source operated at an acceleration voltage of 200 kV. For vitrification, Quantifoil R1.2/1.3 400 mesh grids were overlaid with a thin layer of carbon film and glow discharged. 3  $\mu$ l of mTORC1 ( $\sim 0.02$  mg/ml) was adsorbed to a grid, and the grid was blotted and frozen in liquid ethane using a Vitrobot (FEI). Specimens were examined using a Gatan 626 cryo-holder on a Tecnai F20 electron microscope equipped with a field emission electron source (FEI) operated at 200 kV. Additional details of specimen preparation and data collection are described in the Supplemental Experimental Procedures.

### Image Processing

Details are described in the Supplemental Experimental Procedures.

## SUPPLEMENTAL INFORMATION

Supplemental Information includes Supplemental Experimental Procedures and four figures and can be found with this article online at doi:10.1016/j.molcel.2010.05.017.

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